OM nucleic

Run on:

Sequence:

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Inticum acetivum (blead wheat)

Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatorbyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Spermatorbyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae; Triticeae; Triticum.

1 (bases 1 to 1111)

S Gautier, M.F., Indrai, T. and Joudrier, P. Promoter of thioredoxine TaTrxh2 in wheat

Promoter of thioredoxine TaTrxh2 in wheat

INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE

OS Triticum aestivum (common wheat)

PN JP 2002543844-A/2

PP 24-DEC-2002

PP 17-MAY-2090

PP 17-MAY-1999 FR 99/66231

PR 18-MAY-1999 FR 99/66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAT: 17-JUL-2003
                                                                                                                                                                                                   Pan trogl
Pan trogl
Danio rer
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Drosophil
Zebrafish
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Sus scrof
Pan trogl
  Mus muscu
Human DNA
Sequence
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Pan trogl
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Zea mays
Zea mays
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Sequence
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AC147781
CQ466587
CQ466587
CQ46521
CQ467148
AR542148
AR5210616
AY702552
CQ58506
AC014359
AC147655
AC13854
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AC151884
AC151884
AC151887
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BD263890
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/mol_type="genomic DNA"
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100.0%; Pred. No. 0;
ive 0; Mismatches
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Triticum aestivum (bread wheat)
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AC147655
AC147655
CR788316
AP002352
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AR554285
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AF210616
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CQ585068
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AL929231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0
Matches 1111; Conservative
  2.1 18745

2.1 188285

2.0 1842

2.0 1144

2.0 2.0 1154

2.0 24935

2.0 22270

2.0 24935

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    DEFINITION
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KEYWORDS
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AUTHORS
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JOURNAL
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AC128496 Rattus no
AL77222 Mouse DNA
                                                                                               August 30, 2005, 15:16:40; Search time 5144 Seconds (without alignments) 10465.347 Million cell updates/sec
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AC019327 Homo sapi
AC027290 Homo sapi
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                                                                                                                                                                                       1 gaagtcagaaggccgttcag.......ccgagaagagagagagagag 1111
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AX047681
AX009762
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BX901914
AC021823
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                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                       nucleic search, using sw model
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AL772222
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AC092642
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BD263889
AX047681
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Gapop_60.0 , Gapext 60.0
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seq length: 200000000
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2.3 228676
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Total number Word size :

Searched:

Minimum DB Maximum DB

Database

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Result 8 9

Db 1081 AGGGTGCTTGCCGAGAAGAGAGAGAGAGAGAGAGAGAGAG	AX047682 AX047682 LOCUS LOCUS AX047682 LOCUS ENTER CONTROL OF SET 15-DEC-2000 ACCESSION AX047682 ACCESSION AX047682.1 GI:11876717	KEIWOKUS SOURCE Triticum aestivum (bread wheat) ORGANISM Triticum aestivum Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,		JOUKNAL PATENT: WO 0070065-A Z Z3-NOV-2000; FEATURES LOCATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) SOURCE 1. 1111	/organism="Triticum aestivum" /mol_type="unassigned DNA" /db_xref="taxon:4565"	Query Match Best Local Similarity 100.0%; Score 1111; DB 6; Length 1111; Best Local Similarity 100.0%; Pred. No. 0; Matches 1111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	OY 1 GAAGTCAGAAGGCCGTTCAGAATTGTTGGAGGACTCGAAAAAAAGAAGGGGGGGCCCAGGC 60	QY 61 AGACGACGGGGATGTGCCTGTTCCTTGGCGAGGCGTCTAGGTTTGGCAGCCGCGC 120	QY 121 CGCTTTTCTCCTTGGGTGGGGGGGGGGGGCTCCCCGGGTTTGGGCCGCAATTTTTTACAT 180 L21 CGCTTTCTCCTTGGGTGGGCGCGCGAGCTCCCCCGAGTTTGAGCCGCAATTTTTTACAT 180	OY 181 TTTATGGCGATGGCGTTTATCTAGGCGTCTGGGAGGGTACATTTGAAGATGT 240	QY 241 CCACCAACTCCAAACCGACAACCCTGTATCTGAGCATGCCTCATGCCTCCTTCATGCC 300	Oy 301 TCCCTTTGGGTGAGTCATGTGCCCTTGGCGGGGGGTGGCTTCCCGTTTAGAGCAGTAT 360	QY 361 AATAAGTCCTAGTCAGCTATAAGATGTTCCACATCAGCAANTCCTTAAACTGGAGG 420	QY 421 AGAAAGAAAGTAGGAGTGAGAGGGGGTGTGGCGTTCGTCAATCGCTAACGATAGCACAA 480 Db 421 AGAAAGAAAGTAGGAGTGAGAAAGGGCGTCGGCGTTCGTCAATCGCTAACGATAGCACAA 480	QY 481 GCTCCCATGGAATCGAGCCAACACGGACAATGACTAAAGGCAAACGCCAGCCA	QY 541 ATCAGTATGCCTTTCTTGGATCTTTCTTGATGCAAGCATTAAATACTATAGCTAATCTA 600	Qy 601 CAGCCAGTTTATATAAACAGGCTATATAGCTGACCTGGCAGTGCTATAGAGCCGGCA 660
1 GAAGTCAGAAGGCCGTTCAGAATTGTTGGAGGACTCGAAAAAAAA			241 CCACCAACTCCAAACCGACAACCCTGTATCTGAGCATGCCTCATGCCTCTCTTCATGCC 300	301 TCCCTTTGGGTGAGGTCATGTGCCCTTGGCGGGGGGGGTGCCCGTTTAGAGCAAGTAT 360	361 AATAAGTCCTAGTCAGCTGCTATAAGATGTTCCACATCAGCAAATCCTTAAACTGGAGG 420 	421 AGAAAGAAAGAGAGAGAGGGGGGCGCGCTTCGTCAATCGCTAGCGATAGCAAA 480 	481 GCTCCCATGGAATCGAGCCAACATGCACACACACAATGACTAAAGGCAAAGGCAAGCC 540 	541 ATCAGTATGCCTTTCTCGCATCTTTCTTCATGCAAGCATTAAATACTATAGCTAATCTA 600 	601 CAGCCAGTTTATTATATAACAGGCTATATAGCTGACCTGGCAGTGCTATAGAGCCGGCA 660 	661 GCCGGCTCTTCTATTAGCTTTGCTCTTATGGCTACATCTGTGAGCAGTCGATTGATT	721 AAACAAAAICGGGGGTTCAGCAAGICGGAATGAATTTCGGCTCATCACTCATTGTCG 780 	781 IGGGCCTCACGCGTATTCGCCTAACCGTGTTTGAATCAGACCTCACGAAGCCACGGCTC 840	841 CAGCGACCGTTCACCACGTCAGCTAAAAAAAAAAAAAAA	901 CATCTGAACCGTTCAACAGCCCCACGTAATTTCGCGCACCAGCAAAGGGCATATCCGTCA 960 	961 TAGCGAGCGCATAAATICTGATICCTGCCTGCCGGACAATITATCTITGGGAGGC 1020 	1021 GGGCCGGGATTGGAGGAGGAGCCACAAGGCAACAAAGTGCGCGTGAGAAATCAACA 1080 	1081 AGCGGTGCTTGCCGAGAAGAGAGAGAG 1111

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I"=meineoro/	/mol_type="g /db_xref="ta ORIGIN	Query Match Best Local Similarity 100.0%;	2	1 GAAGTCAGAAGGCCGTT	Qy 61 AGACGACGGGGGCATGT	61	Qy 121 CGCTTTTCTCCTTGGTGG 	181	181	Qy 241 CCACCAACTCCAAACCGAC 	Qy 301 TCCCTTTGGGTGAGGTCAT	Db 301 TCCCTTTGGGTGAGGTCAI	Qy 361 AATAAGTCCTAGTGGCTG	Db 361 AATAAGTCCTAGTCAGCTG		DD 421 AGAAAGAAAGTAGGAGTGA	Qy 481 GCTCCCATGGAATCGAGCC	Db 481 GCTCCCATGGAATCGAGCC	541		601	601	661	661 GCCGGCTCTT	721	721 AAACAAC	18/	Db 781 TGGGCCTCACGCGTATTCC	Qy 841 CAGCGACCCGTTCACCACC	841		Db 901 CATCTGAACCGTTCAACAC
601 CAGCCAGTTTATTATATAAACAGGCTATATAGCTTGACCTGGCAGTGCTATAGAGCCGGCA 660	GCCGGCTCTTCTATTAGCTTTTGCTCTTATGGCTACATCTGTGAGCAGTCGATTGATT	661 GCCGGCTCTTCTATTAGCTTTGCTCTTATGGCTACATCTGTGTGAGCAGTCGATTGATT	721 AAACAAATCCGGGCGTTCAGCAAGTCGGAATGAATTTCGGCTCATCATTGTCG 780	781 TGGGCCTCACGGGTATTCGCCTAACCGTGTTTGAATCAGACCCTCACGAAGCCACGGCTC 840	81 1666CCTCACGCGTTCACCCTAACCGTGTTTGAATCAGACCCTCACGAAGCCACGGCTC	CAGCGACCCGTTCACCACGTCAGCCTAAAAAAAAAAAAA	901 CATCTGAACCGTTCAACAGCCCCACGTAATTTCGCGACCAGCAAGGGCATTATCCGTCA 960	901 CATCTGAACCGTTCAACAGCCCCACGTAATTTCGCGCACCAGCAAAGGGCATATCCGTCA 960	961 TAGCGAGCGCATAAATTCTGATTCCTGCCTGCCCGCACAATTTATCTTTGGGGAGGC 1020	GGGCCGGGATTGGAGGAGGCCGACAAGGCAACAAGTGCGCGTGAGAATCAACA	1021 GGGCCGGGATTGGAGACAGAGCCCACAAGGCAACAAAGTGCGCGTGAGAAATCAACA 1080	AGCGGTGCTTGCCGAGAGAGAGAGAGAGAGAGAGAGAGAG	1081 AGCGGTGCTTGCCGAGAAGAGAGAGAGAG 1111	RESULT 3	Z	BD263889	YEROLON BLEGOSOS: 1 21.5507.0057 KEYWORDS JP 2002543844-A/L. SOURCE Triticum aestivum (bread wheat)	H	bukalyota, Vilalipianae, strepropijaa, bmolyopijaa, itaniopijaa, Spermatophyta; Magnoliophyta, Liliopsida; Poales; Poaceae; Pooldeae; Triticeae; Triticum.	REFERENCE 1 (bases 1 to 2687) AUTHORS Gautier, M.F., Ihorai, T. and Joudrier, P.	<pre>IIILE Promoter of thioredoxine TaTrxh2 in wheat JOURNAL Patent: JP 2002543844-A 1 24-DEC-2002;</pre>	INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE COMMENT OS Triticum aestivum (common wheat)	PN JP 2002543844-A/1 PD 24-DEC-2002	PF 17-MAY-2000 JP 2000618471 PR 17-MAY-1999 FR 99/06231	PI MARIE FRANCOISE GAUTIER, TANIA IHORAI, PHILIPPE JOUDRIER PC C12N15/09, A01H5/00, C12N5/10//(C12N5/10, C12R1:91), C12N15/00, PC	C12N5/00, PC (C12N5/00,C12R1:91)	CC Promoter of thioredoxine TaTrxh2 in wheat FH Key Location/Qualifiers	FT exon (1112). (1231) FT intron (1232). (2203)	FT exon (2204). (2326) FT intron (2327). (2420)	FT exon (2421). (2558) FT CDS (1112). (1231)	FT CDS (2204). (2326) FT CDS (2421). (2558).	FEATURES Location/Qualifiers source 1. 2687

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TRECTETTCCTTGGCGAGGCGTCTAGCTTTGGCAGCCGCCGC 120
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Triticum aestivum"
genomic DNA"
axon:4565"
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%; Pred. No. 0;
0; Mismatches
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9 9 9

540 540

		Db 961 TAGGAGGCATAAATTCTGCTGCCTGCCGGCCAATTTTTTTT	TAESULT 5 TAES762 LOCUS TOCUS
Qy 961 TAGCGAGCGCATAAATTCTGATTCCTGCCTGCCGGACAATTTATCTTTGGGAGGC 1020 Db 961 TAGCGAGCGCATAAATTCTGATTCCTGCCTGCCGGACAATTTATCTTTGGGAGGC 1020 Db 1021 GGGCGGGATTGGAGACAGAGCCAAAGGCAACAACAAAGTGCGGTGAGAAATCAACA 1080 Db 1021 GGGCGGGATTGGAACAGAGCCACAAGGCAACAACAACAAAGTGCGCGTGAGAAATCAACA 1080 Qy 1081 AGCGGTGCTTGCCGAGAACAAGAGCAACAACAACAACAAAAGTGCGCGTGAGAAATCAACA 1080 Qy 1081 AGCGGTGCTTGCCGAGAAGAGAGAGAGAG 1111 Db 1081 AGCGGTGCTTGCCGAGAAGAGAGAGAGGAG 1111	RESULT 4 AX047681 AX047681 LOCUS ACCESSION AX047681 AX047681 ACCESSION AX047681 AX04	ORIGIN ORIGIN Query Match Query Match Query Match Query Matches 1111; DB 6; Length 2687; Matches 1111; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 GAAGTCAGAAGGCCGTTCAGAATTGTTGGAGGACTCGAAAAAAAA	

Gaps

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BX901914 228676 bp DNA linear HTG 10-OCT-2004 Danio rerio clone DKEY-27F18, WORKING DRAFT SEQUENCE, 17 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Sctinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 228676)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 222727 bases at least Q40
Consensus quality: 223391 bases at least Q40
Consensus quality: 224176 bases at least Q20
Insert size: 227076; sum-of-contigs
Unsert size: 222615; 5.7% error; agarose-fp
Quality coverage: 6.94x in Q20 bases; sum-of-contigs Quality
coverage: 7.21x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 * NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                    Length 629
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                                                                                                                       DB 8; Le
6.6e-06;
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Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                        1080 AAGCGGTGCTTGCCGAGAGAGAGAGAGAGAGAG 1111
                                                                                                                                                                                                                                                                                               58 AAGCGGTGCTTGCCGAGAGAGAGAGAGAGAGAG
                                                                                                                    Query Match 2.9%; Score 32; DB Best Local Similarity 100.0%; Pred. No. 6.6 Matches 32; Conservative 0; Mismatches
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AUTHORS
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SOURCE
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Submitted (24-JUL-1998) Cejudo F.J., Instituto de Bioquimica
Vegetal Y Potosintesis, Universidad de Sevilla Y CSIC, Avda Americo
Vespucio s/n, 41092-Sevilla, SPAIN
Location/Qualifiers
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| FTASWCGPCRIMAPIPADIAKKFPAANVENKVDVDELKSIAEQFSVEANPTFLFMKEGD |
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| FTASWCGPCRIMAPIPADIAKKFPAANVENKVDVDELKSIAEQFSVEANPTFLFMKEGD |
| FTASWCGPCRIMAPIPADIAKKFPAANVENKNDVDELKSIAEQFSVEANPTFLFMKEGD |
| FTASWCGPCRIMAPIPADIAKKFPAANVENKNDVDELKSIAEQFSVEANPTFLFMKEGD |
| FTASWCGPCRIMAPIPADIAKKFPAANVENKNDVDELKSIAEQFSVEANPTFLFMKEGD |
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| FTASWCGPCRIMAPIPATATAANVENKNDVDELKSIAEQFSVEANPTFLFMKEGD |
| FTASWCGPCRIMAPIPATATAANVENKNDVDELKSIAEQFSVEANPTFLFMKEGD |
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| FTASWCGPCRIMAPIPATAANVENTATAANVENTATAANVENTATAANVENTATAANVENTATAANVENTATAANVENTATAANVENTATAANVENTATAANVENTATAANVENTATAANVENTATAANVENTATAANVENTATAANVENTATAANVENTATAANVENTATAANVENTATAANVENTATAANVENTATAANVENTATAANVENTATAANVENTATAANVENTATAANVENTATAANVENTATAANVENTATAANVENTATAANVENTATAANVENTATAANVENTATAANVENTATAANVENTATAANVENTATAANVENTATAANVENTATAANVENTATAANVENTATAANVENTATAANVENTATAANVENTATAANVENTATAANVENTATAANVENTATAANVENTATAANVENTATAANVENTATAANVENTATAANVENTATAANVENTATAANVENTATAANVENTATAANVENTATAANVENTATAANVENTATAANVENTATAANVENTATAANVENTATAANVENTATAANVENTATAANVENTATAANVENTATAANVENTA
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Spermatophyta; Magnoliophyta, Liliopsida, Poales, Poaceae,
Pooideae, Triticeae, Triticum.
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Submitted (06-UTJ-2000) Cejudo F.J., Instituto de Bioguimica
Vegetal Y Fotosintesis, Universidad de Sevilla, Avda Americo
Vespucio s/n, 41092-Sevilla, SPAIN
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Serrato, A.J., Crespo, J.L., Florencio, F.J. and Cejudo, F.J. Characterization of two thioredoxins h with predominant localization in the nucleus of aleurone and scutellum cells germinating wheat seeds Plant Mol. Biol. 46 (3), 361-371 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.9%; Score 54; DB 8;
100.0%; Pred. No. 2e-18;
ive 0; Mismatches
                                                                                                                                               organism="Triticum aestivum"
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/gene="thioredoxin H"
462. .466
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Triticum aestivum
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/gene="thioredoxin H"
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thioredoxin H.
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/note="ORF"
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Cejudo, F.J.
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Matches 54; Conservative
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TITLE
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MEDLINE
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KEYWORDS
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                                                                                        FEATURES
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151428: gap of 100 bp

167242: contig of 15814 bp in length

167342: gap of 100 bp

179999: contig of 12657 bp in length

180099: gap of 100 bp

190992: contig of 10893 bp in length

191092: gap of 100 bp

228676: contig of 37584 bp in length
                                                                                                                                 151328: contig of 17192 bp in length 151428: gap of 100 bp 161428: gap of 100 bp
              100 bp
of 13496 bp in length
                                                                124219: Contig of 14394 bp in length
124319: gap of 100 bp
129512: contig of 5193 bp in length
129512: gap of 100 bp
2440 bp in length
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/clone=lib="Dariokey"
1. .10555
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fragment chain: 3"
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109725: contig of
109825: gap of 100
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 contig
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124320
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                  96130
96230
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Dipublished
Chases Ito 146015)
Sirren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F.
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Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T. M., Peterson, K.,
Pierre, N., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N.,
Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
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Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                      ACUZIB23 146015 bp DNA linear HTG 04-APR-2000
HOMO sapiens chromosome 2 clone RP11-169P13 map 2, WORKING DRAFT
SEQUENCE, 22 unordered pieces.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                         Gaps
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Contact sequence tame: 15939
Center project Information
Center project name: 169 P 13
Center clone name: 169 P 13
Center clone name: 169 P 13
Sequencing vector: M13, M77815, 100% of reads
Sequencing vector: M13, M77815 100% of reads
Assembly program: Phrap, version 0.960731
Consensus quality: 135544 bases at least Q30
Consensus quality: 14539 bases at least Q30
Consensus quality: 14539 bases at least Q20
Insert size: 153000; agarose-fp
Insert size: 143915; aum-of-contigs
Quality coverage: 4.1 in Q20 bases; sum-of-contigs
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                                                                                                           Query Match 2.3%; Score 26; DB 2; Length 228676; Best Local Similarity 100.0%; Pred. No. 0.018; Matches 26; Conservative 0; Mismatches 0; Indels 0;
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 2, clone RP11-169P13
191093. .228676
/note="assembly_fragment:02360"
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Web site: http://www-seq.wi.mit.edu
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Homo sapiens (human)
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AC021823.3 GI:7408019
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Direct Submission
Submitted (19-JUL-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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1 (Dases 1 to 152251)
Sulston, J. E. and Waterston, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
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Homo sapiens BAC clone RP11-391P1 from 2, complete sequence
AC092642 AC023761
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Mulvaney, E., Abbott, A., Dixon, R., Dignan, G. and Phillips, A.
The sequence of Homo sapiens BAC clone RP11-391P1
Unpublished (2001)
3 (bases 1 to 152251)
Waterston, R.H.
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127829. .146015
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90350. .102852
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              NOTE: This is a 'working draft' sequence. It currently consists of 22 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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contig of 2932 bp in length

gap of 100 bp

contig of 3419 bp in length

gap of 100 bp

contig of 3419 bp in length

gap of 100 bp

contig of 4143 bp in length

gap of 100 bp

contig of 6433 bp in length

gap of 100 bp

contig of 6433 bp in length

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contig of 6433 bp in length

gap of 100 bp

contig of 4793 bp in length

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0: contig of 3520 bp in length
7: gap of 100 bp
1: contig of 4978 bp in length
9: gap of 100 bp
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contig of 1525 bp in length
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contig of 1429 bp in length
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contig of 2304 bp in length
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contig of 3324 bp in length
contig of 3324 bp in length
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102525: gap of 100 bp
114466: contig of 11514 bp in length
114566: gap of 100 bp
127728: contig of 113162 bp in length
127728: gap of 100 bp
146015: contig of 18187 bp in length.
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141. .1665
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90349: 0
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Gaps

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'note="match to EST AI038041 (NID:g3277235) ox29h03.x1"
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9534. .9825
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/rpt_family="MaLR"
9284. .9387
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/rpt_family="(TG)n"
11080. .11325
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7956_ .839^
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/rpt_family="Alu"
1695. .2130
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3162 ...3456
/rpt family="Alu"
3325 ...3365
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3759. .4066
/rpt_family="Alu"
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/rpt_family="L1"
7608. .7643
                   rpt_family="MaLR'
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1780. .626°
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'rpt_family="L1"
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9480. .9537
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1524. .1624
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                     Direct Submission (01-MRA-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Sep 18, 2001 this sequence version replaced gi:14916226.
                                                                               Submitted (18-SEP-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA (bases 1 to 152251)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Data from AC062033, AC061960, and AC021823 was used to finish this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The clone sequenced to the left is RP11-544E11, 2000 bp overlap; the clone sequenced to the right is RP11-710J17, 2000 bp overlap. Actual end of this clone is at base position 19440 of RP11-710J17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence of AC023761 has been incorporated into AC092642.
Location/Qualifiers
1. .152251
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                                                                                                                                                                                                                                                                     Center: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                               NEIGHBORING SEQUENCE INFORMATION:
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/db_xref="taxon:9606"
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/rpt_family="MalR"
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                     4 (bases 1 to 152251)
Waterston, R.H.
Direct Submission
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BX001022 160804 bp DNA linear VRT 11-OCT-2003
Zebrafish DNA sequence from clone CH211-243019, complete sequence.
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Danio rerio
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
Insert size: 154454; sum-of-contigs
Insert size: 158561; 1.9% error; agarose-fp
Quality coverage: 11.18x in Q20 bases; sum-of-contigs Quality
Coverage: 10.90x in Q20 bases; agarose-fp
                                                                                           * NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary, Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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                                                                                                                                                                                                                                             33656: contig of 33656 bp in length
33756: gap of 100 bp
51099: contig of 17343 bp in length
51199: gap of 100 bp
60096: contig of 8897 bp in length
60196: gap of 100 bp
85968: contig of 25672 bp in length
85968: contig of 25672 bp in length
116591: contig of 30623 bp in length
116691: gap of 100 bp
147668: contig of 30977 bp in length
147768: gap of 100 bp
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116692. .147668
1note="assembly_fragment:01071"
147769. .155054
/note="assembly_fragment:02238"
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1. .33656
|note="assembly_fragment:00001
fragment chain:1"
33757. 51099
|note="assembly_fragment:02384
fragment chain:1"
51200. .60096
fragment chain:2"
60197 .36566
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/db_xref="taxon:7955"
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BX001022.9 GI:37652295
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BX001022/c
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Danio rerio clone DKEY-146H10, WORKING DRAFT SEQUENCE, 7 unordered
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Submitted (07-0CT-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. B-mail enquiries:
zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Oct 9, 2004 this sequence version replaced gi:52313301.
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Cyptiniformes, Cyptinidae, Danio.
(pases 1 to 155054)
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    note="match to EST T84526 (NID:9712878) yd53a07.rl"
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HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
Danio rerio (zebrafish)
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Chemistry: Dye-terminator; 100% of reads
Consensus quality: 153838 bases at least Q40
Consensus quality: 153985 bases at least Q30
Consensus quality: 154096 bases at least Q20
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100.0%; Pred. No. v.
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18502. 18571
19347. 19607
/rpt_family="L2"
20299. 20328
/rpt_family="AT_rich"
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22507. .22594
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1504. .21678
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                            .2315. .12336
'rpt_family="AT_rich"
.5388. .15522
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/rpt_family="AcHobo"
22644. .23228
                                                                         /rpt_family="L2"
15624. 15788
/rpt_family="(TG) n"
15831. 15898
/rpt_family="(TG) n"
                                                                                                                                                                                            family="Alu"
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0821. .21353
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.5934. .16232
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1356. .21468
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0300.
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Best Local Similarity
Matches 24; Conserva'
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BX927299
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KEYWORDS
SOURCE
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VRT 06-DEC-2003
                                                                      Danio rerio (zebrafish)
Danio rerio
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
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                                                                                                                                                                                                                                                                                                    Context: zfish-helpdanger.ac.uk
Context: zfish-helpdanger.ac.uk
Context: zfish-helpdanger.ac.uk
Context: zfish-helpdanger.ac.uk
Context project Information
Consensus quality: 18489 bases at least Q40
Consensus quality: 185061 bases at least Q20
Consensus quality: 185152 bases at least Q20
Insert size: 185217; sum-of-contigs
Insert size: 210440; 9.8% error; agarose-fp
Quality coverage: 9.78x in Q20 bases; sum-of-contigs Quality
coverage: 8.61x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       * NOTE: This is a 'working draft' sequence. It currently
consists of 1 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces
is believed to be correct as given, however the sizes
of the gaps between them are based on estimates that have
provided by the submittor.
This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.

I 182277: contig of 185217 bp in length.
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                                                                                                                                                                                                                                                           Center code: SC
Web site: http://www.sanger.ac.uk
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 185217)
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/organism="Danio rerio"
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/db_xref="taxon:7955"
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/clone_lib="CHORI-211"
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BX649502
                                                   Ellwood, M
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                           REFERENCE
                                                      AUTHORS
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                                                                                                                                                                                                                                                                                                                                                  During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, SMSSRROT; Tr., TREMBL; WP:, WORNPEP; Information on the WORNPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep Clone-derived Zebrafish pUC subclones occasionally display inconsistency over the length of monourcleotide A/T runs and conserved TA repeats. Where the which it is found the longest good quality representation will be
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BX927400
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                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi,
                                                                                                 Submitted (11-OCT-2003) Wellcome Trust Sanger Institute, Hinxton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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HTG; HTGS PHASE2; HTGS ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
Danio rerio (zebrafish)
Danio rerio
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CH211-243019 is from a CHORI-211 BĀC library
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100.0%; Pred. No. 0.24;
tive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                           Center code: SC
Web Bite: http://www.sanger.ac.uk
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 160804)
                                                                                                                                                                                                                                                                                                            Contact: zfish-help@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="CH211-243019"
/clone_lib="CHORI-211"
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                                                                              Direct Submission
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Best Local Similarity
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                                                Giselle, H
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BX927400/c
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AUTHORS
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Gaps

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Submitted (04-APR-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. B-mail enquiries:
zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Apr 6, 2004 this sequence version replaced gi:46200415.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Insert size: 262069; sum-of-contigs
Insert size: 249466; 4.6% error; agarose-fp
Quality Coverage: 8.81x in Q20 bases; sum-of-contigs Quality
coverage: 9.36x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  * NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8720: contig of 8720 bp in length
8820: gap of 100 bp
34299: contig of 25379 bp in length
34299: gap of 100 bp
61537: contig of 27238 bp in length
61537: contig of 27238 bp in length
82441: gap of 100 bp
113867: contig of 31146 bp in length
113867: gap of 100 bp
117899: contig of 3146 bp in length
117899: gap of 100 bp
117899: gap of 100 bp
117053: gap of 100 bp
159533: contig of 2464 bp in length
17053: gap of 100 bp
232102: contig of 21840 bp in length
1919393: gap of 100 bp
235112: contig of 3510 bp in length
235114: gap of 100 bp
256314: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 260222 bases at least Q40
Consensus quality: 260911 bases at least Q30
Consensus quality: 261370 bases at least Q20
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/note="assembly_fragment:00210

fragment chain:1"

8821. .34199

/note="assembly_fragment:01606

fragment_chain:1".
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/note="assembly_fragment:01245
fragment_chain:1"
                                                                                                                                                                                                                                                 Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                   Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
------ Project Information
Center project name: zK54Kl3
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Cypriniformes; Cyprinidae; Danio.
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/db xref="taxon:7955"
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1. .263169
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                          (bases 1 to 263169)
                                                                                     Direct Submission
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                                                       Sims.S.
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AUTHORS
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                                                                                                                                                                                               COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (1.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL: Sw: SWISSEROT: Tr:, TREMBL; WP:, WORNPEP: Information on the WORNPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep Clone-derived zebrafish pUC subclones occasionally display inconsistency over the length of monouncleotide A/T runs and conserved TA repeats. Where this is found the longest good quality representation will be
                                                                                                                                                                                                                                                                                                                                                              During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA linear HTG 05-APR-2004
Danio rerio clone DKEY-54K13, *** SEQUENCING IN PROGRESS ***, 12
unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml DKEY-204F11
is from a Zebrafish BAC library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Waterman (Stephen Johnson
                                               Direct Submission
Submitted (06-DEC-2003) Wellcome Trust Sanger Institute, Hinxton,
Gambridgeshire, CB10 ISA, UK. B-mail enquiries:
zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Dec 6, 2003 this sequence version replaced gi:38201304.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Danio rerio
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Repeat names beginning 'Dr' were identified by the Recon repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lab, WashU). For further information see
                                                                                                                                                                                                                            Center: Wellcome Trust Sanger Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Danio rerio"
/mol_type="genomic DNA"
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/clone="DKEY-204F11"
/clone_lib="DanioKey"
                                                                                                                                                                                                                                                                               Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
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HTG; HTGS PHASE1.
Danio rerio (zebrafish)
  (bases 1 to 247387)
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                             AUTHORS
TITLE
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* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
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AUTHORS
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Ratcus.

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Ruzny, D.Marie., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J.,

Anjen, C., Allen, H., Alabrooks, S., Amin, A., Angulano, D.,

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Claveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,

Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,

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Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,

Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.,

Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M.,

Gebregeorgis, E., Geer, K., Ganda, R., Gardy, M., Guerra, W.,

Gunaratne, P., Haaland, M., Hamil, C., Hamilton, C., Hamilton, K.,

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Hernandez, R., Howells, S., Hulk, S., Hume, J., Idlebird, D., Jackson, A.,

Jackson, L., Jang, H., Johnson, B., Johnson, R.,
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Rattus norvegicus clone CH230-444D9, WORKING DRAFT SEQUENCE, 3
unordered pieces.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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100.0%; Pred. No. 0.24;
tive 0; Mismatches 0; Indels 0;
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                                                                                                     /note="assembly_fragment:01994
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HTG; HTGS_PHASE1; HTGS_DRAFT; 1
Rattus norvegicus (Norway rat)
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Best Local Similarity 100.
Matches 24; Conservative
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KEYWORDS
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Unitert Duminablou
Submitted (19-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Nov 19, 2002 this sequence version replaced gi:23907748.
The sequence in this assembly is a combination of BAC based reads
and whole genome shockyn sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Bach contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
contigs within a contig-scaffold that consist entirely of whole
genome shockun sequence reads. Both end sequences and whole genome
shotgun sequence contigs will be indicated in the feature
Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Luiu, J., Liu, W., Liu, W., Lodon, P., Longacre, S., Lopez, J., Liu, M., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensuhewai., Loulseged, H., Lozado, R.J., Lu, X., Ma, J., Mandensuhewai., Loulseged, H., Lozado, R.J., Martinez, E., Mangum, A., Mansqum, B., Mapua, P., Martin, K., Martinez, E., Mandiney, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Mandiney, S., McLeod, M.P., McNeill, T.Z., Menen, E., Mandiney, S., McLeod, M.P., McNeill, T.Z., Menen, E., Mandiney, S., McLeod, M.P., McNeill, T.Z., Menen, E., Mandiney, S., Morris, K., Morris, S., Munidaea, M., Murphy, M., Nair, L., Nankeris, C., Neal, D., Newton, N., Nguyen, N., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Puazo, M., Qinicoz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Rives, C., Rodkey, T., Rojas, A., Rose, M., Richards, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, B., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Taplor, P., Taylor, C., Taylor, Y., Taylor, Y., Taylor, Y., Wals, M., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Waight, D., Wright, R., Wullson, R., Walsk, R., Weisk, M., Weisk, R., Shang, C., Wailson, R., Waisson, T., Yoon, L., Yoon, U., Yu, F., Zhou, X., Zhou, X., Zhou, X., Zhou, X., Zhou, Y., Waisson, Mederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H., M., Thomasion, M., Thomasion, M., Meissy, R., Smith, D.R., Waisson, M., Maisson, R., Maitson, R., Weisk, R., Smith, D.R., Waisson, M., Maisson, R., Maitson, R., Waisson, R., Waisson,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Baylor College of Medicine
Center code: BCM
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2 (bases 1 to 291544)
Worley,K.C.
Direct Submission
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NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                     1 288506: contig of 288506 bp in length
5507 288606: gap of unknown length
6607 289399: contig of 1343 bp in length
650 290049: gap of unknown length
650 291544: contig of 1495 bp in length
6050 291544: contig of 1495 bp in length.
6050 10011fiers
6050 10011fiers
7050 1
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complement(187560..188645)
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clone_end:Sp6
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/note="wgs end_extension
clone_end:Sp6"
195009. . 196648
/note="wgs end_extension
clone_end:Sp6"
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/note="wgs_end_extension
clone_end:T7"
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/note="clone_boundary
clone_end:T7
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Search completed: August 30, 2005, 18:23:47 Job time : 5165 secs

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Abv21724 Human pro Abv27546 Human pro Abk88932 Human CD1 Abk88932 Human CD1 Abk897557 Human Can Abx64451 Human ben Abk64451 Human pol Abg58941 Human pol Abg8957 EST clone Ach22705 Human car Ade47440 Human car Ade7440 Human car Ads7458 Human car Ads75258 Sereast ca Acn52902 Breast ca Acn52938 Tumour-as Acn5293 Soybean o Acn52938 Tumour-as Acn5293 Soybean o Acn52938 Sumour-as Acn5293 Humour-as Acn52934 Humour-as Acn5294 Humour-as Acn5

score:

Title: Perfect #

Sequence:

nucleic

Run on:

Scoring table:

Word size :

Database

Searched:

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Wheat, TaTrxh2; thioredoxin; promoter; gene expression; transgenic plant; monocotyledon; plant cell; seed; amylaceous albumen; ds.
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/function= "possible regulator of gene expression in
response to abscisic acid"
/note= "present in thioredoxin h gene promoter sequences
from tobacco and rice"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= b
/label= Gibberellic acid_response element
/label= arbertic acid_response element
gibberellic acid"
561. .569
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//abel= Gibberellic acid_response_element
//function= "regulates gene expression in response
gibberellic acid"
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/teg= a
/notes = promoter region is specifically claimed"
550. .558
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/label= bzip_motif
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/bound_moiety= "GCN4-like protein'
/label= GCNA-like_box
                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                               ABK64451
ABK4868
ABK4868
ABC58941
AAV89657
ACH22705
AACH22705
AACH22238
AAK52328
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                                       ABD33381
ADQ97557
ABZ08670
              ABV27546
ABK88932
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                             (first entry)
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4740
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 protein_bind
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  AAC84132;
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Ab186452 Human ova
Ab186187 Human ova
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Abl8631 H
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Abl86321 H
Abl8631 B
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Abl6218 H
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Abd74749 H
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Compugen Ltd
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                 GenCore version (c) 1993 - 2005
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                                                                        nucleic search, using sw model
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ABL810390
AAV86132
AAC24900
AAT11551
AAT1289
ABV22589
ABV2269
ABV2269
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Gapop_60.0 , Gapext 60.0
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Maximum DB seq length: 2000000000
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             expression,
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0
                                                                     Length 2687;
 to control gene expression in transgenic plants (particularly monocotyledons) or plant cells, especially for seed-specific particularly in the amylaceous albumen
                                              Sequence 2687 BP; 638 A; 626 C; 690 G; 733 T; 0 U; 0 Other;
                                                                                           Indels
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                                                                     DB 5;
                                                                   Query Match
100.0%; Score 1111;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1111; Conservative 0; Mismatches
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              *tag= g
dound_moiety= "basic helix-loop-helix transcription
actor"
                                                                                                                           function= "involved in aleurone layer-specific gene
                                                                                                                                                                                               *tag= k
function= "involved in aleurone layer-specific gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New promoter from a wheat thioredoxin gene, useful for controlling transgene expression in plants, provides seed-specific expression.
                                                                                                                                                                                                                                           *tag= 1
bound moiety= "Sp1 transcription factor"
bound moiety= "Sp1 transcription factor"
bound 1231
1047. .1231
                                                                   *tag= h
'bound moiety= "leucine zipper proteins"
/label= bzip_motif
1001. .1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (5'site:YES, 3'site:NO)
                                              label= bHLH_recognition_motif
                                                                                                                                                                                                                                                                                                                                            product= "thioredoxin h2"
note= "CDS contains introns"
232. .2202
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note= "TATA-like box
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gene= "TaTrxh2"
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429. .2687
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/number= 3
2558. .2687
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2584. .2589
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2203. .2325
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1002. .1008
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1021. .1028
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/*tag= q
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   906.
                                                          24. .927
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/number=
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protein_bind
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                                                       protein_bind
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540 540 900 900 99 999 720 720 780 780 840 840 900 900 960

480

420

960

Pred. No.

Best Local Similarity

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The present invention describes a composition (I) comprising: carriers and immunostimulants; and a polypeptide (II) of a ovarian tumour polypeptide encoded by a polypeptide (III) having a cDNA sequence (SI) from the 10912 nucleotide sequence as given in AB177023 to AB187934, (III) encoding (II) having a sequence (S2), a T cell population of (II), cartison presenting cells that express (II). (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to (SI) can be used for detecting ovarian cancer in a patient's biological sample preferably serum or ovarian tissue. The method comprises contacting a biological sample from a patient with (IV), detecting the amount of polymucleotide hybridising to (IV) and comparing the amount to a preferrably by polymucleotide phybridising to (IV) is detecting ovarian cancer in the patient, where the amount of polymucleotide phybridising to (IV) is detected preferably by polymucleotide phybridising (I) comprising (III) and/or (II) is useful for stimulating and/or expanding T cells specific for an ovarian tumour protein comprising Contacting T cells specific for an ovarian cuseful in design and preparation of ribozyme molecules for inhibiting expression of the tumour polypepides and proceines in tumour cells; and the collar and proceines and proceines in tumour cells; and the collar and proceines and proceines in tumour cells; and the collar and proceines and proceines in tumour cells.
TAGCGAGCGCATAAATTCTGATTCCTGCCTGCCTGCCGGACAATTTATCTTTGGGGAGGC 1020
                         TAGCGAGCGCATAAATTCTGATTCCTGCCTGCCTGCCGGACAATTTATCTTTGGGGAGGC 1020
                                                                            GGGCCGGGATTGGAGACAGAGCCCACAAGACAACAAGAGTGCGCGTGAGAAATCAACA.1080
                                                                                                                  1021 GGGCCGGGATTGGAGACAGAGCCCACAAGGCAACAACAAGTGCGCGTGAGAAATCAACA 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Composition for therapy and diagnosis of ovarian cancer comprising polypeptide of a ovarian tumor polypeptide, polynucleotide encoding polypeptide, antibody specific to polypeptide or T cell expressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                Human ovarian cancer related cDNA clone SEQ ID NO:9430.
                                                                                                                                                                                    AGCGGTGCTTGCCGAGAGAGAGAGAGAGAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 9430; 489pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               library using well known techniques
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jones R;
                                                                                                                                                                                                                                                                                                         ABL86452 standard; cDNA; 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-MAY-2001; 2001WO-US017756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-MAY-2000; 2000US-0207484P
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                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200192581-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                       17-MAY-2002
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2.0%; Score 22; DB 6; Length 141;

Query Match

Seguence 141 BP; 58 A; 26 C; 46 G; 11 T; 0 U; 0 Other;

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The present invention describes a composition (I) comprising: carriers and immunostimulants, and a polymedide (II) of a ovarian tumour concled by a polymuclectide (III) having a cDNA sequence (SI) from the 10912 nuclectide sequences as given in ABL77021 to ABL87934, (III) encoding (II) having a sequence (S2), a T cell population of (II), or antigen presenting cells that express (II). (I) has cytostatic cativity. An oligonuclectide (IV) that hybridises to (SI) can be used for detecting ovarian cancer in a patient's biological sample preferably cample from a patient with (IV), detecting the amount of polymuclectide chybridising to (IV) and comparing the amount to a predetermined cutoff cylubra and thereby detecting ovarian cancer in the patient, where the amount of polymuclectide hybridising to (IV) is detected preferably by colymerase chain reaction (PCR). (I) comprising (III) and/or (II) is cuseful for simulating and/or expanding T cells specific for an ovarian tumour protein comprising contacting T cells with (III) or (II) is cuseful in design and preparation of ribozyme molecules for inhibiting expression of the tumour polypeptides and proteins in tumour cells; and to isolate a full length gene from a suitable library e.g., a tumour cDNA
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                                                                                                                                                                                                                                                                                                                      Human; ovarian cancer; ovarian tumour; cytostatic; gene;
                               Indels
                                                                                                                                                                                                                                                                                    Human ovarian cancer related cDNA clone SEQ ID NO:9165.
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Pred. No. 2;
Mismatches
              red. No. 2;
Mismatches
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                                                                                     98 AGCCTAAAAAAAAAAAAAAAA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jones R;
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100.0%; Pre-
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                                                               862 AGCCTAAAAAAAAAAAAAA
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                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Algate PA, Harlocker SL,
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                              22; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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                                 Matches
                                                                                                                                                   RESULT 3
ABL86187
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Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.

Human ovarian cancer related cDNA clone SEQ ID NO:9926.

17-MAY-2002 (first entry)

ABL86948;

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The present invention describes a composition (I) comprising: carriers and immunostimulants, and a polypeptide (II) of a ovarian tumour propertied encoded by a polynucleotide (III) having a cDNA sequence (S1) from the 10912 nucleotide sequence sa given in ABL77023 to ABL87334, (III) encoding (III) having a sequence (S2), a T cell population of (II), or antigen presenting cells that express (II). (I) has cyrostatic activity. An oligonucleotide (IV) that hybridises to (S1) can be used for detecting ovarian cancer in a patient's biological sample preferably searuh or ovarian tissue. The method comprises contacting a biological sample from a patient with (IV), detecting the amount of polynucleotide hybridising to (IV) and comparing the amount to a predetermined cutoff hybridising to (IV) is detecting ovarian cancer in the patient, where the amount of polynucleotide hybridising to (IV) is detected preferably by polymerase chain reaction (PCR). (I) comprising (III) and/or (II) is useful for stimulating and/or expanding T cells specific for an ovarian tumour protein comprising contacting T cells with (III) or (III) is useful in design and preparation of ribosyme molecules for inhibiting useful in design and preparation of ribosyme molecules for inhibiting to constacting a tumour cells; and to isolate a full length gene from a suitable library e.g., a tumour cDNA library using well known techniques
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polypeptide of a ovarian tumor polypeptide, polynucleotide encoding polypeptide, antibody specific to polypeptide or T cell expressing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                Human ovarian cancer related cDNA clone SEQ ID NO:9299.
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tive 0; Mismatches
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                                                                                          ABL86321 standard; cDNA; 154 BP.
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                                                                                                                                                                                                                                                                     (first entry)
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Best Local Similarity
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                                                                                                                                                                                    ABL86321;
RESULT 4
                                                    ABL8632:
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Composition for therapy and diagnosis of ovarian cancer comprising polypeptide of a ovarian tumor polypeptide, polynucleotide encoding polypeptide, antibody specific to polypeptide or I cell expressing

굓 Jones

Harlocker SL,

Algate PA,

WPI; 2002-122075/16.

29-MAY-2001; 2001WO-US017756.

WO200192581-A2. Homo sapiens

06-DEC-2001.

26-MAY-2000; 2000US-0207484P.

(CORI-) CORIXA CORP.

Claim 1; SEQ ID NO 9926; 489pp; English.

polypeptide

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The present invention describes a composition (I) comprising: carriers and immunostimulants; and a polypeptide (II) of a ovarian tumour composition encoded by a polymuclectide (III) having a cDNA sequence (SI) from the 10912 nuclectide sequences as given in ABL77023 to ABL87334, (III) encoding (II) having a sequence (S2), a T cell population of (II), or antigen presenting cells that express (II). (I) has cytostatic critical presenting cells that express (II). (I) has cytostatic critical presenting cells that express (II). (I) has cytostatic critical cartivity. An oligonuclectide (IV) that hybridies to (SI) can be used for cerum or ovarian tissue. The method comprises contacting a biological sample from a patient with (IV), detecting the amount of polynuclectide critical comparing the amount to a predetermined cutoff value and thereby detecting ovarian cancer in the patient, where the amount of polynuclectide hybridising to (IV) is detected preferably by collymerase chain reaction (PCR). (I) comprising (III) and/or (II) is cuseful for stimulating and/or expanding T cells specific for an ovarian tumour protein comprising contacting T cells with (III) or (III) is useful in design and preparation of ribozyme molecules for inhibiting cexpression of the tumour polypeptides and proteins in tumour cells; and contacting well known techniques allocated in brary using well known techniques
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    163 AGCCTAAAAAAAAAAAAAAAA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADL62118 standard; DNA; 1074
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Matches 22; Conservative
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ID ADL621:
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Gaps

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22; Conservative

Matches

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ABL86948 standard; cDNA; 213 BP.

RESULT 5 ABL86948 ID ABL86

ABL10390/c ID ABL10390 standard; cDNA; 24935 BP.

ABL10390;

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The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancerous) ovarian cells. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the encoded by the markers, antibodies that selectively bind to the oblypeptides. a method of inhibiting ovarian cancer in a patient at risk of developing ovarian cancer involving inhibiting expression of a gene corresponding ovarian cancer comprising providing to calls of the patient an antisense oligonuclectide complementary to a marker of the invention and a method of traating a patient an antisense oligonuclectide complementary to a marker in a control non-ovarian cancer sample. A difference between the invention. The marker in a patient sample and a normal level of expression of a marker in a patient sample and a normal level of expression of the marker in a control non-ovarian cancer. The level of expression of a corresponds to a secreted protein or to a transcribed protein or its portion. The level of expression of the marker is assessed by detecting the presence of the protein or protein fragment is detected using an antibody that specifically binds with the corresponding to the marker. The presence of a transcribed comparising the presence of a transcribed comparising the presence of a transcribed comparising the marker, under stringent conditions. The patient which involves detecting expression of the marker in a patient conditions and comparising the level of expression of ovarian cancer in a patient which involves detecting expression. The method at a subsequent time and comparising the level of expression of the marker is a sequence represente a human ovarian cancer. Day marker of the propression of the marker is a sequence represente a human ovarian cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.
Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 20330; 106pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0207124P.
2000US-0211940P.
2000US-0216820P.
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                                                                                                                                                                              WO200170979-A2
                                                                                         Homo sapiens
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EST clone H165.
             AAV86132;
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                                                                 Gaps
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Sequence 1074 BP; 194 A; 278 C; 290 G; 300 T; 0 U; 12 Other;
                           0%; Score 22; DB 5; Length 1074; J.0%; Pred. No. 2.2;
                                                               0; Indels
                                       100.0%; Preα ...
'... 0; Mismatches
                                                                                                867 AAAAAAAAAAAAAAAACTGTT 888
                                                                                                                               427 AAAAAAGAAAAAAAACTGTT 406
                                                               22; Conservative
                               Query Match
Best Local Similarity
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Matches

ઠે 셤 RESULT

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Expressed sequence tag; secreted protein; haematopoiesis regulator; tissue growth; activin; inhibin; tumour invasion suppressor; EST; human; chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis; receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher enkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABIA16176, ABIA16176, ABIA1617), expressed DNA ABRA2072). The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                               detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                            Drosophila melanogaster expressed polynucleotide SEQ ID NO 25652.
                                                                                                        developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 24935 BP; 7255 A; 5321 C; 5280 G; 7079 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 25652; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 2.0%; Score 22i. Db Best Local Similarity 100.0%; Pred. No. 2.4 Matches 22i, Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                    Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       872 AAGAAAAAAAACTGTTCAATC 893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B
                                                                                                                                                                                                                                                                                                                                                                    Li PWD,
                                                                                                                                                                                                                                                       23-MAR-2001; 2001WO-US009231.
                                                                                                                                                                                                                                                                                      23-MAR-2000; 2000US-0191637P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAV86132 standard; cDNA; 377
                                                                                                                                                                                                                                                                                                   11-JUL-2000; 2000US-00614150
                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid
genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-APR-1999 (first entry)
                                                                                                                                                          Drosophila melanogaster,
                                                                                                                          pharmaceutical; gene;
                                                                                                                                                                                                                                                                                                                                                                   Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                     (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; ABB66287
                                                                                                                                                                                         WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                interactions.
                                              26-MAR-2002
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AAV86132/c
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The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intext 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid for diagnosing and treating cervical cancer and for assessing and detecting compounds for treating the cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
                                                                                   New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.
                                                                                                                                                                             Claim 1; SEQ ID NO 28975; 71pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 403 BP; 141 A; 68 C; 60 G; 128 T; 0 U; 6 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cervical cancer marker nucleic acid 2825.
Duclert A, Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Preq. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.9%; Score 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 579; 1051pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            863 GCCTAAAAAAGAAAAAAA 883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163 GCCTAAAAAAAAAAAAAAAA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Berger A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expression and secretion vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-DEC-1999; 99US-0171350P.
14-MAR-2000; 2000US-0189115P.
12-MAY-2000; 2000US-0203791P.
09-UUN-2000; 2000US-0210600P.
21-JUL-2000; 2000US-0220114P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH71551 standard; cDNA; 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-DEC-2000; 2000WO-US03312.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Deeds J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-375006/39.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAH71551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schlegel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents an expressed sequence tag (EST), and is a polynucleotide of the invention. The polynucleotides of the invention are all secreted EST sequences isolated from a variety of human tissue sources. The EST sequences and proteins encoded by them are predicted to have useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity, haematopoiesis regulating activity, tissue growth activity, activity, chemotratic/Chemokinetic activity, activity, chemotratic/Chemokinetic activity, activity, activity, activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, tumour inhibition activity. The EST sequences are also stated to be useful for gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                proteins - derived from e.g. testes, brain, ovary,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                       Treacy M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 21; DB 2; Length 377;
                                                                                                                                                                                                                                                                       Racie LA, Merberg D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 377 BP; 89 A; 88 C; 76 G; 124 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human secreted protein 5' EST, SEQ ID NO: 28975.
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                                                                                                                                                                                                                                                                                                                                                                             New polynucleotides encoding human secreted human blood, kidney, foetal lung, placenta, pituitary, retina and colon cDNA libraries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.0%; Pred. No. 6.8
Matches 21; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                       Lavallie ER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    863 GCCTAAAAAAAAAAAAAA 883
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 132; 633pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAC24900 standard; cDNA; 403 BP
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                                                                                                                                   98WO-US006954
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                                                                                                                                                                               97US-00835913
                                                                                                                                                                                                                                                                                            Spaulding V, Agostino MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                         (GEMY ) GENETICS INST INC
                                                                                                                                                                                                                                                                       Mccoy JM,
                                                                                                                                                                                                                                                                                                                                        WPI; 1999-070076/06.
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    Ното варіепв
                                              WO9845435-A2
                                                                                                                                                                               10-APR-1997;
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                                                                                                                                      10-APR-1998;
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                                                                                          15-0CT-1998
                                                                                                                                                                                                                                                                       Jacobs K,
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Gaps

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DB 3; Length 403; 6.8; 0; Indels

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Gaps

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0; Indels

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neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynaccological; antibacterial; gene therapy; neural; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; proliferative disorder; wound; infectious disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prostate cancer associated gene sequences, referred to as prostate cancer antigens, useful for treatment, prevention, and diagnosis of disorders
              The invention relates to novel genes (AAH68727-AAH73383) associated with dervical cancer with cytostatic activity. The nuclaic acids and encoded polypeptides are useful: to assess if a patient is afflicted with cervical cancer or has a pre-malignant condition; to monitor the progression of cervical cancer or a premalignant condition in a patient, and to select and/or assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The nucleic acids may also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer; prostate cancer antigen; detection; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Human prostate cancer antigen nucleotide sequence SEQ ID NO:630.
                                                                                                                                                                              1.9%; Score 21; DB 4; Length 621;
100.0%; Pred. No. 6.9;
                                                                                                                                               Sequence 621 BP; 273 A; 63 C; 47 G; 238 T; 0 U; 0 Other;
                                                                                                                                                                                            1 Similarity 100.0%; Pred. No. 6.9
21; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 1072-1073; 2338pp; English.
                                                                                                                                                                                                                                         864 CCTAAAAAAAAAAAAAAAAA
                                                                                                                                                                                                                                                          CCTAAAAAAGAAAAAAAAAC 621
                                                                                                                                                                                                                                                                                                                                              AAF16195 standard; cDNA; 1097 BP
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                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                such as prostate cancer.
                                                                                                                   useful for gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-587513/55.
                                                                                                                                                                                             Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAB56992.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                         13-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                          AAF16195;
                                                                                                                                                                                                                                                                     601
                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human;
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The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to
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5
              represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant
                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gapa
                                                                                                                                                                                                                                                                                                                                                                         Plant; bacterial infection; fungal infection; viral infection; rice;
disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
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                                                         Sequence 1097 BP; 301 A; 204 C; 201 G; 389 T; 0 U; 2 Other;
                                                                                     DB 3; Length 1097;
7;
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100.0%; Pred. No. 7.2;
tve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2000 BP; 632 A; 370 C; 326 G; 672 T; 0 U; 0 Other;
                                                                                                                   Indels
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Zhu
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Whitham S, Xie
                                                                                    1.9%; Score 21; DB
100.0%; Pred. No. 7;
ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SYGN ) SYNGENTA PARTICIPATIONS AG.
                                                                                                                                                863 GCCTAAAAAAAAAAAAAA 883
                                                                                                                                                                            162 GCCTAAAAAAGAAAAAAA 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            867 AAAAAAAAAAAAAAACTGT 887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Pr
tive 0;
                                                                                                                                                                                                                                                      ADA72818 standard; DNA; 2000 BP
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S, Tao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-JUN-2001; 2001WO-IB001105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-JUN-2001; 2001WO-IB001105.
                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                  Best Local Similarity 100.
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         illustrate the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen W, Co
F, Quan S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-175290/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2003000898-A1
                                                                                                                                                                                                                                                                                                                                                Rice gene, SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa.
                                                                                                                                                                                                                                                                                                                 20-NOV-2003
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                             invention
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Katagiri
                                                                                                                                                                                                                                                                                                                                                                                            ds.
               AAB57303
                                                                                                                                                                                                                                                                                   ADA72818;
                                                                                     Query Match
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AAF15566 to AAF16505 encode the human prostate cancer associated proteins, called prostate cancer antigens, given in AAB56363 to AAB57302. The prostate cancer antigens can have neuroprotective, cytostatic, cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal, nephrotropic, antiinfective, gynaecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polynuclectides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative

AAH72880/c

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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether protection is afflicted with prostate cancer. (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a therapy for inhibit in prostate cancer in a patient; (d) assessing the efficacy of an inhibit prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cancer in a patient; (f) assessing the prostate cancer has metastasized in a patient; (g) determining whether prostate cancer has metastasized in a patient; (h) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
                                                                                                                                                                                                                                                                                                                                                                           Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
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                                                                                                                                                                                                                                                                                                      Monahan JE
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16-MAR-2000; 2000US-0189862P.
                                                                                                                                                                 2000US-0207454P.
2000US-0211314P.
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                                                                                        20-FEB-2001; 2001WO-US005171.
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25-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cervical cancer with cytostatic activity. The nucleic acids and encoded polypoptides are useful: to assess if a patient is afflicted with cervical cancer or has a pre-malignant condition; to monitor the progression of cervical cancer or a premalignant condition in a patient; and to select and/or assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The nucleic acids may also be useful for gene therapy
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                                                                                                                                                                                                             Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
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100.0%; Pred. No. 7.2;
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                                                      AAH72880 standard; cDNA; 2170 BP
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12-MAY-2000; 2000US-0203791P.
09-JUN-2000; 2000US-0210600P.
21-JUL-2000; 2000US-0220114P.
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RESULT 14 ABV22589/c

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PR 25-MAY-2000; 2000US-021314P.
PR 19-JUN-2000; 2000US-0219307P.
PR 11-DEC-2000; 2000US-0219007P.
PR 13-DEC-2000; 2000US-0255281P.

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X (MILL.) MILLENNIUM PREDICTIVE MEDICINE INC.

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PI Schlegel R, Endege WO, Monahan JE;

XX

Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer. useful for detecting presence of prostate cancer, stage of prostate cancer.

XX

Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer.

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Claim 1; Page 5153; 11750pp; English.

XX

C The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ARV00010-ARV62213) of the aptient is afflicted with prostate cancer; (b) monitoring the efficacy of a therapy for inhibiting prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (c) assessing the aggressiveness or indolence of prostate cancer in a patient; (c) assessing the aggressiveness or indolence of prostate cancer in a patient; (n) assessing the aggressiveness or indolence of prostate cancer in a patient; (n) assessing the aggressiveness or indolence of prostate cancer in a patient; (n) assessing the aggressiveness or indolence of prostate cancer in a patient; (n) assessing the aggressiveness or indolence of prostate cancer in a patient; (n) assessing the aggressiveness or indolence of prostate cancer in a patient; (n) assessing the aggressiveness or indolence of prostate cancer in a patient; (n) assessing the aggressiveness or indolence of prostate cancer in a patient; (n) assessing the aggressiveness or indolence of prostate cancer in a patient; (n) assessing the aggressiveness or indolence of prostate cancer in a patient; (n) assessing the about the patient of the patient o
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Gaps

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Sequence 15057, A Sequence 14724, A Sequence 14724, A Sequence 120940, Sequence 15104, A Sequence 15104, A Sequence 80011, A Sequence 80012, A Sequence 148215, Sequence 148215, Sequence 1377, App Sequence 1377, App Sequence 3377, App Sequence 3377, App Sequence 3377, App Sequence 3377, App Sequence 34824, App
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Sequence 14043, A Sequence 12373, A Sequence 11808, A Sequence 11310, A Sequence 5369, App Sequence 4, Appli Sequence 60407, A Sequence 60822, A Sequence 74691, A Sequence 74890, A Sequence 74891, A Sequence 74891, A		CES RELATING TO CANDIDA ALBICANS	gth 249; Indels 0; Gaps 0;		ASSOCIATED OF DETECTION AND USES THEREOF
4 US-09-949-016-14043 4 US-09-949-016-113373 4 US-09-949-016-11808 4 US-09-949-016-13388 4 US-09-252-991A-5369 3 US-08-479-089A-4 4 US-09-949-016-6821 4 US-09-949-016-68221 4 US-09-949-016-68222 4 US-09-949-016-74693 4 US-09-949-016-74693 4 US-09-949-016-74693 4 US-09-949-016-74693 4 US-09-949-016-74693 4 US-09-949-016-74693 4 US-09-949-016-74894 5 US-09-949-016-74894 6 US-09-949-016-74894	ALIGNMENTS	US/09248796A et al C ACID AND AMINO ACID SEQUENCES RELATING IAGNOSTICS AND THERAPEUTICS -02-12 US 60/074,725 -13 US 60/096,409 -13	0%; Score 22; DB 4; Len .0%; Pred. No. 0.77; 0; Mismatches 0;	Gadaaaaaact 885 Gadaaaaact 87	6 NOWN GENES E, METHODS 016
20 1.8 312470 20 1.8 63624 20 1.8 636591 19 1.7 555 19 1.7 601 19 1.7 601		SULT 1 1-02-248-796A-9416/C 1-02-248-796A-9416/C Sequence 9416, Application US/09248796A Patent No. 6747137 GENERAL INFORMATION: TITLE OF INVENTION: NUCLEIC ACID AND AMINO TITLE OF INVENTION: FOR DIAGNOSTICS AND T FILE REFERENCE: 107196.132 CURRENT APPLICATION NUMBER: US/09/248,796A CURRENT FILING DATE: 1999-02-12 PRIOR FILING DATE: 1998-02-13 PRIOR PILING DATE: 1998-02-13 PRIOR FILING DATE: 1998-08-13 NUMBER OF SEQ ID NOS: 28208 LENGTH: 249 TYPE: DAA ORGANISM: Candida albicans	cch 2.0%; al Similarity 100.0%; 22; Conservative	864 CCTAAAAAAAGAAAAAAAAAACT 	RESULT 2 US-09-49-016-119414/C Sequence 119414, Application US/0994901 Patent No. 6812339 GENERAL INFORMATION: TITLE OF INVENTION: POLYMORPHISMS IN K TITLE OF INVENTION: WITH HUMAN DISEAS. FILE REFERENCE: CLO01307 CURRENT APPLICATION NUMBER: US/09/949, CURRENT FILING DATE: 2000-04-14 PRIOR PILING DATE: 2000-10-03 PRIOR FILING DATE: 2000-10-03 PRIOR FILING DATE: 2000-10-03 PRIOR FILING DATE: 2000-10-03 PRIOR FILING DATE: 2000-09-08 PRIOR FILING DATE: 2000-09-08 NUMBER OF SEQ ID NOS: 207012 SOFTWARE: FRAEVESQ FOF WINGOWS VERSION
00000 00 000000000000000444444 00010000001000010040		RESULT 1 US-02-248-796, Sequence 94 Patent No. GENERAL INF APPLICANT; TITLE OF II TITLE OF II FILE REFER CURRENT FI PRIOR APPL PRIOR APPL PRIOR PILI PRIOR	Query Match Best Local Matches 2	8 9 1	RESULT 2 US-09-949-016 Sequence 11 Sequence 11 Patent No. FAPPLICALINI TITLE OF 1 TITLE OF 1 TITLE OF 1 TITLE OF 1 FILE REPER CURRENT AN CURRENT AN CURRENT AN PRIOR APPI PRIOR FILL PRIOR FILL PRIOR PILL PRIOR FILL PRIOR

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RESULT 5
US-09-949-016-14724/c
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ORGANISM: Human
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Sequence 15077, Application US/09949016

Sequence 15077, Application US/09949016

GENERAL INFORMATION:

APPLICANT: VENTER, U. Craig et al.

ITLLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

ITLLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOO1307

CURRENT FILING DATE: 2000-04-14

PRIOR PLLING DATE: 2000-10-20

PRIOR PLLING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FeastSeQ for Windows Version 4.0

SEQ ID NO 15057

LENGTH: 51403
                                                                                                                                                                                                                                                                                                                                                        Sequence 119415, Application US/09949016

Batent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENITON: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENITON: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CLOU3307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-0-0-08
NUMBER OF SEQ ID NOS: 207012
SOFFTMARE: PESELSCA for Windows Version 4.0
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                                                                                                                                   DB 4; Length 601;
0.77;
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                                                                                                                     2.0%; Scc...
100.0%; Pred. No. ...
0; Mismatches
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Best Local Similarity 100.
Matches 22; Conservative
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                        ; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-119414
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ORGANISM: Human
FEATURE:
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SEQ ID NO 119414
LENGTH: 601
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USE OF JULY APPLICATION US/09949016

| Sequence 14724, Application US/09949016
| Patent No. 6812339
| GENERAL INFORMATION:
| APPLICANT: VENTER, J. Craig et al. |
| TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF; |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF; |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF; |
| FILE REPRESENCE: C100130, 1007 |
| PRIOR APPLICATION NUMBER: 00/231, 768 |
| PRIOR PILING DATE: 2000-10-20 |
| PRIOR PILING DATE: 2000-10-3 |
| PRIOR PILING DATE: 2000-10-3 |
| PRIOR FILING DATE: 2000-09-08 |
| NUMBER OF SEC ID NOS: 207012 |
| SOFTHAME: FREASES FOR Windows Version 4.0 |
| SEQ ID NO 14724 |
| LENGTH: 250352
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; Sequence 28975, Application US/09513999C
; Patent No. 6783961
; GRENEAL INFORMATION:
; APPLICANT: Duclett, A.
; APPLICANT: Duclett, A.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REPERENCE: 59.US2.REG
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR PILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 28975
; LENGTH: 403
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                                                                                                              Query Match 2.0%; Score 22; DB 4; Length 51403; Best Local Similarity 100.0%; Pred. No. 0.82; Matches 22; Conservative 0; Mismatches 0; Indels (
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CTHER INFORMATION: n = A,T,C or G
US-09-949-016-15057
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; LOCATION: (1)...(250352)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14724
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FEATURE

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US-09-949-016-15104/c

Sequence 15104, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VEWTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR PELING DATE: 2000-10-03

PRIOR PELING DATE: 2000-10-03

PRIOR PELING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PSESEED for Windows Version 4.0

SED ID NO 15104

LENGTH: 33908
                      PAPELICANT: VENTER,

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REPERENCE: CLAOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PILING DATE: 2000-10-20

PRIOR PELING DATE: 2000-10-90

PRIOR PELING DATE: 2000-09-08

NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER: PASICEO FOR Windows Version 4.0

SEQ ID NO 169966

LENGTH: 601

TYPE: DNA

ORGANISM: Human

US-09-949-016-169866
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100.0%; Pred. No. 2.5;
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Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 21; Conservative 0; Mismatches
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Matches 21; Conservative 0; Mismatches
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US-09-949-016-16536
S. Sequence 16536, Application US/09949016
Parent No. 6812339
GENERAL INFORMATION:
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ORGANISM: Human
PEATURE:
NAME/KEY: misc_feature
LCCATION: (1)...(33908)
OTHER INFORMATION: n = A,T,C or G
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US-09-949-016-120940

Sequent No. 6812339

GENERAL INFORMATION:

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOOL307

CURRENT APPLICATION NUMBER: 00/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PELING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR PLILING DATE: 2000-10-03

PRIOR PLILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PASESEQ for Windows Version 4.0

LENGTH: 601
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US-09-949-016-169986/c
; Sequence 169986, Application US/09949016
; Patent No. 6812339
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LOCATION: 332
OTHER INFORMATION: h=a or c or t
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; OTHER INFORMATION: v=a or c or g
US-09-513-999C-28975
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                                                     LOCATION: 56 TOTHER INFORMATION: rag or
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LOCATION: 254
OTHER INFORMATION: w=a or
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OTHER INFORMATION: n=a,
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LOCATION: 271
OTHER INFORMATION: n=a,
FEATURE:
NAME/KEY: misc_feature
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFRENCE: CL001307
CURRENT APPLICATION NUMBER: U6/9/949,016
CURRENT ELING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PELING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PSESEE FOR Windows Version 4.0
LENGTH: 601
APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,756

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FRAFISEQ for Windows Version 4.0
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Pred. No. 7.9;
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2-09-949-016-80010/c
; Sequence 80010, Application US/09949016
; Patent No. 6812339
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i OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16536
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Best Local Similarity 100.
Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Human
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ORGANISM: Human
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LENGTH: 114139
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Sequence 80011, Application US/09949016 Partent No. 6812339 GRERAL INFORMATION: PAPLICANT: VENTER, J. Craig et al.

RESULT 12 US-09-949-016-80011/c

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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION WUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR PPLICATION NUMBER: 60/241,755
PRIOR PLILNG DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PASLSEQ for Windows Version 4.0
SEQ ID NO 80011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 136288, Application US/09949016
Fatent No. 6812339
GENERAL INFORMATION:
APPLICANT VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
FILE REPERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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100.0%; Pred. No. 7.9;
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100.0%; Pred. No. 7.9
:ive 0; Mismatches
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Best Local Similarity 100...
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Best Local Similarity 100.0
Matches 20, Conservative
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US-09-949-016-80012
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US-09-949-016-80011
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KENULI ARBOLIS APPLICATION US/09949016

Sequence 148215, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-20
PRIOR PLILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NO 148215
LENGTH: 601
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1.8%; Score 20; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 20; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 7.9;
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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FESTSEQ for Windows Version 4.0
SEQ ID NO 134288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              875 AAAAAAAACTGTTCAATCA 894
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Best Local Similarity 100.0
Matches 20; Conservative
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; ORGANISM: Human
US-09-949-016-148215
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; ORGANISM: Human
US-09-949-016-136288
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Db 335 ĠĠĀĠĠĀĀĀĠĀĀĀĠĀĀĠĠĀ 316 Search completed: August 30, 2005, 19:38:33 Job time: 231 secs

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Wed Aug 31 10:30:03 2005

GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

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Sequence 9430, Ap
Sequence 9165, Ap
Sequence 9299, Ap
Sequence 9926, Ap
Sequence 20330, A
Sequence 20330, A
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                                                                  August 30, 2005, 16:45:56 ; Search time 859 Seconds (without alignments) 8462.599 Million cell updates/sec
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cgn2_6/ptodata/1/pubna/PCT NEW PUB.seq:*
cgn2_6/ptodata/1/pubna/USO6_NEW PUB.seq:*
cgn2_6/ptodata/1/pubna/USO6_NEW PUB.seq:*
cgn2_6/ptodata/1/pubna/USO6_NEW PUB.seq:*
cgn2_6/ptodata/1/pubna/USO8_NEW PUB.seq:*
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US-10-741-600-17952
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US-09-867-701-9165
US-09-867-701-9299
US-09-867-701-9926
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nucleic search, using sw model
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Maximum DB seq length: 200000000
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Perfect score:
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8 21 1.9 9 21 1.9 10 21 1.9 11 21 1.9 11 21 1.9 11 21 1.9 11 21 1.9 11 21 1.9 11 21 1.9 11 21 1.9 11 21 1.9 11 21 1.9 11 21 1.9 11 21 1.9 12 21 1.9 12 21 1.9 13 21 1.9 14 21 1.9 18 32 21 1.9 22 21 1.9 24 21 1.9 25 21 1.9 26 20 1.8 31 20 1.8 32 21 1.9 28 20 1.8 31 20 1.8 32 21 1.9 24 21 1.9 25 21 1.9 26 20 1.8 36 20 1.8 37 20 1.8 38 20 1.8 39 20 1.8 34 20 1.8 34 20 1.8 34 20 1.8 34 20 1.8 35 20 1.8 36 20 1.8 37 20 1.8 38 20 1.8 39 20 1.8 39 20 1.8 31 20 1.8 34 20 1.8 35 20 1.8 36 20 1.8 37 20 1.8 38 20 1.8 39 20 1.8 39 20 1.8 31 20 1.8 31 20 1.8 32 20 1.8 33 20 1.8 34 20 1.8 35 20 1.8 36 20 1.8 37 20 1.8 38 20 1.8 39 20 1.8 39 20 1.8 39 20 1.8 30 20 1.8 31 20 1.8 32 20 1.8 34 20 1.8 35 20 1.8 36 20 1.8 37 20 1.8 38 20	imi '
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; Batent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Aglate, Paul A.
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: COMPOSITIONS OF OVARIAN CANCER; FILE REFERENCE: 2.1012.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; UNRER OF SIGO ID NOS: 10912
; SOFTWARE: FastSEQ for Windows Version 4.0
; TENTER OF 100 1005.10912
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Patent No. US20020132237A1
GENERAL INFORMATION:
APPLICANT: Aglate, Paul A.
APPLICANT: Jones, Robert
APPLICANT: Harlocker, Sugan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS OF OVARIAN CANCER
FILE REFERENCE: 210121.497
Sequence 9430, Application US/09867701
Patent No. US20020132237A1
GENERAL INFORMATION:
APPLICANT: Jones, Paul A.
APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 2.0%; Score 22; DB 9; Length 141; Best Local Similarity 100.0%; Pred. No. 0.62; Matches 22; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9430
LENGTH: 141
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; ORGANISM: Homo sapien
US-09-867-701-9165
                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapien
US-09-867-701-9430
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US-09-867-701-9299
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                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
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Sequence 20330, Application US/09814353
Sequence 20330, Application US/09814353
Publication No. US20030165831A1
GENERAL INFORMATION:
APPLICANT: Lee, John
APPLICANT: Lillie, Jamea
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, TITLE OF INVENTION: THERAPY OF OVARIAN CANCER, TITLE OF INVENTION: THERAPY OF OVARIAN CANCER, TITLE OF INVENTION THERAPY OF OVARIAN CANCER, TITLE OF INVENTION UNMBER: US/09/814,353
CURRENT APPLICATION NUMBER: US 60/191,031
PRIOR FILING DATE: 2000-03-21
PRIOR PELICATION NUMBER: US 60/211,940
PRIOR PELING DATE: 2000-06-25
PRIOR PELING DATE: 2000-06-15
PRIOR PELING DATE: 2000-06-15
PRIOR PELING DATE: 2000-07-07
PRIOR PELING DATE: 2000-07-07
PRIOR PELING DATE: 2000-07-07
PRIOR PELING DATE: 2000-07-25
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Sequence 9226, Application US/09867701

Patent No. US2002013237A1

GAPERRAL INFORMATION:

APPLICANT: Aglate, Paul A.

APPLICANT: Jones, Robert

APPLICANT: Hallocker, Susan L.

TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER

TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER

FILE REPERENCE: 210121.497

CURRENT FILING DATE: 2001-05-29

NUMBER OF SEQ ID NOS: 10912

SOFTWARE PALICAND OF SEQ FOR WINDOWS Version 4.0

SEQ ID NO 9926

LENGTH: 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
2.0%; Score 22; DB 9; Length 213;
Best Local Similarity 100.0%; Pred. No. 0.63;
Matches 22; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                  Length 154;
                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                  Query Match 2.0%; Score 22; DB 9; Best Local Similarity 100.0%; Pred. No. 0.62; Matches 22; Conservative 0; Mismatches
CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9299
LENGTH: 154
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US-09-867-701-9299
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US-09-867-701-9926
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US-09-867-701-9926
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Sequence 101740, Application US/10425115
; Sequence 101740, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 101740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ## Sequence 46223

## Sequence 46223, Application US/10085783A

## Publication No. US20040037841A1

## Publication No. US20040037841A1

## Publication No. US20040037841A1

## PELICANT: ChondroGene Inc.

## APPLICANT: ChondroGene Inc.

## PELICANT: ChondroGene Inc.

## TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis

## PILER REFERENCE: 4231/2002

## CURRENT FILING DATE: 2002-02-28

## PRIOR APPLICATION NUMBER: US 60/305,340

## PRIOR PILING DATE: 2001-07-13

## PRIOR PILING DATE: 2001-03-12

## PRIOR PILING DATE: 2001-03-12

## PRIOR PILING DATE: 2001-03-28

## NUMBER OF SEQ ID NOS: 58994

## SOFTWARE: PatentIN Version 3.2

## ENGINE PATENTION NUMBER: US 60/271,955

## NUMBER OF SEQ ID NOS: 58994

## SEQ ID NO 46223

## LENGTH: 261
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  ; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46223
; LENGTH: 261
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-46223
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Matches 21; Conservative
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US-10-425-115-101740/c
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ORGANISM: Zea mays
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US-10-085-783A-46223
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| OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-741-600-17952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 17952, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SEQ ID NO 17952
; SEQ ID NO 17952
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TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis FILE REFERENCE: 4231/2002
CURRENT APPLICATION NUMBER: US/10/242,535A
CURRENT FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 10/085,783
PRIOR FILING DATE: 2002-02-28
PRIOR FILING DATE: 2001-07-13
PRIOR PILING DATE: 2001-07-13
PRIOR PILING DATE: 2001-07-13
PRIOR PILING DATE: 2001-07-13
PRIOR PILING DATE: 2001-03-12
PRIOR FILING DATE: US 60/275,017
PRIOR PILING DATE: US 60/275,017
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                                                                                                                                                                                                                                                                                                                                                                            Query Match 2.0%; Score 22; DB 10; Length 1074; Best Local Similarity 100.0%; Pred. No. 0.69; Matches 22; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                         NAME/KEY: misc_feature; LCATION: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 968, 1074; OTHER INFORMATION: n = A,T,C or G
US-09-814-3153-20330
PRIOR APPLICATION NUMBER: US 60/257,672
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
SSCTWARE: FastSEQ for Windows Version 4.0
LENGTH: 1074
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Publication No. US20040013663A1
GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
APPLICANT: Liew, C.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              867 AAAAAAGAAAAAAAAACTGTT 888
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                                                                                                                                                                                       ORGANISM: Homo sapiens
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US-10-741-600-17952/c
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US-10-242-535A-46223
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us-lu-u2/-624-169396, Application US/10027632
; Sequence 169366, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US 60/218,006
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR PAPLICATION NUMBER: US 60/198,676
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR PLING DATE: 1909-09-28
; PRIOR FILING DATE: 1999-09-28
; PRIOR FILING DATE: 1999-09-38
; PRIOR FILING DATE: 1999-09-69
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE FREESEQ FOR Windows Version 4.0
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                                                                                                                                                                                      1.9%; Score 21; DB 13; Length 828; 100.0%; Pred. No. 2.4; tive 0; Mismatches 0; Indels
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA101
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: ECT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR PLING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 169396
LENGTH: 828
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Patent No. US20020111681A1
GENERAL INFORMATION:
APPLICANT: Craig Rosen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 AAAAAAGAAAAAAAAACTGT 138
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Best Local Similarity
Matches 21; Conserv
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Matches 21; Conserv
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                                                                                                                                       US-10-027-632-169396
                                                                                   TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-925-300-630/c
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LFNGTH: 828
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Wu, Pei
APPLICANT: Wu, Wei
APPLICANT: APPLICANT: Wu, Wei
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: VUNDER: US/10/437,963
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 3058
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GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE OF INVENTION NUMBER: US 60/128,066
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-109-28
PRIOR FILING DATE: 1999-09-28
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1.9%; Score 21; DB 19; Length 614;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 21; Conservative 0; Mismatches 0; Indels
                                                       1.9%; Score 21; DB 20; Length 542;
100.0%; Pred. No. 2.4;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Clone ID: PAT_MRT4530_102776C.1
US-10-437-963-3058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 169396, Application US/10027632 Publication No. US20020198371A1
                                                                                                                                                                                                                                                                                                                                                 ; Sequence 3058, Application US/10437963; Publication No. US20040123343A1; GENERAL INFORMATION:
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                                                                                                                                                                   863 GCCTAAAAAAAAAAAAAA 883
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                                                                                                                                                                                                                     50 GCCTAAAAAAAAAAAAAA 30
                                                                                                                 Conservative
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ORGANISM: Oryza sativa
                                                            Query Match
Best Local Similarity
Matches 21; Conserv
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        US-10-425-115-101740
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Sequence 88377, Application US/10437963
; Sequence 88377, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
    APPLICANT: La Rosa, Thomas J.
    APPLICANT: Cao, Yongwei
    APPLICANT: Cao, Yongwei
    APPLICANT: Wu, Weii
    APPLICANT: Wu, Weii
    APPLICANT: Barbazuk, Brad
    APPLICANT: Li, Ping
    TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
    FILE REFERENCE: 38-21(5321)B
    CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
    NO SEQ ID NOS: 204966
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1.9%; Score 21; DB 19; Length 1420;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 21; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                     Query Match 1.9%; Score 21; DB 9; Length 1097; Best Local Similarity 100.0%; Pred. No. 2.5; Matches 21; Conservative 0; Mismatches 0; Indels
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: NAME/KEY: unsure

: LOCATION: (1)..(1420)

: OTHER INFORMATION: unsure at all n locations

: FEATURE:

: OTHER INFORMATION: Clone ID: PAT_MRT4530_84521C.1

US-10-437-963-85377
                                                                                                                                                  ; NAME/KEY: misc feature
; LOCATION: (13)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-300-630
                                                                                                                                                                                                                                                                                                                                                                                        162 GCCTAAAAAAGAAAAAAAA 142
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NUMBER OF SEQ ID NOS: 1890
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 630
LENGTH: 1097
                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
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ORGANISM: Oryza sativa
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US-10-437-963-85377
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Search completed: August 30, 2005, 19:52:58 Job time : 860 secs

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CA593541 Wpalc.pk0
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                                                                                      August 30, 2005, 16:27:35; Search time 4253 Seconds (without alignments) 9943.429 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                  34239544 segs, 19032134700 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
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                                                          OM nucleic - nucleic search, using sw model
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CA712930
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Gapop_60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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Match Length DB
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gb_est2::
gb_est3::
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gb_est6::
gb_gs81::
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Perfect score:
Sequence:
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CKI58740 FGASO4003 CA702286 wdklc.pko BA223826 BA223826 BR005555 WRE3567 H BR406240 WHR5367 H BR406240 WHR5369 D BA273554 BA273554 BA17101004 WHR5360 F CA717478 wdk4-c.pko CA597581 wpalc.pko BA320546 BA320546 CD930486 GR45.11H CD8741149 FGASO4298 ALR21149 FGASO2298 ALR223651 BA223651 BA223851 BA223651 BA223851 BA223651 BA223286 BA223661 BA223286 BA2236073 BA223286 BA2236073 BA223286 BA2236073 BA223286 BA2236073	S mRNA linear BST 11-JUL-2003	ivam com crome recreacy.	in plant c	he framework of the french (http://www.genoplante.com .fr). "	ength 509;	G IIIGEIS C CAPE	AGAG 1111 AGAG 99
889 7 CKIS6740 418 6 CA702286 557 4 BJ223826 628 5 BQ805515 353 2 BR406240 563 4 BJ273554 565 5 BJ101004 567 6 CA717478 614 6 CA597581 630 4 BJ273554 630 4 BJ220546 644 6 CD874126 1141 7 CK211149 1141 7 CK211149 156 2 BE419352 633 4 BJ228073 577 4 BJ224045 887 7 CK188744 137 4 BJ22280	ALIGNMENT S09 bp	:32551389 vum (bread wheat) vum idiplantae; Streptc Magnoliophyta; Lili	partnership fre	en generated in ti "amme 'Genoplante' e-info.infobiogen ialifiers "Triticum aestivum "RNA" recital" raxon:4565" 22106K05"	ib="AZO2" 9%; Score 99; DB 6 .0%; Pred. No. 1.4e	CONBELVACIVE OF MISMACCHES OF INDEES OF CONSELVACIVE SAPERGEORGE OF CAPERGEORGE OF CAPERGEORG OF CAPERGEO	AATCAACAAGGGTGCTTGCCGAGAAGAGAGAGAGAGAGAG
22 24 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	CD867573	MANA SEQUENCE. CD867573 GENERAL CD867573.1 GI ENT. Triticum aesti Triticum aesti Triticum aesti Spermatophyta; Pooideae; Triti	1 (bases 1 to 509) Genoplante, a major Genoplante, a major Unpublished (2003) Contact: Genoplante Genoplante 93, rue Henri Rochef Fest: 33 1 69 47 54 0 Fex: 33 1 69 47 54 0	This sequency plant genome and http://orange.com/magnetale.com/magnetale.com/magnetale.com/com/com/com/com/com/com/com/com/com/	/ imilarit	99; COMBETAGLIVE 013 GGGGAGGCGGG 1 GGGGAGGCGGGGCCGG	
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 CD867573 LOCUS		REFERENCE AUTHORS TITLE JOURNAL COMMENT	FEATURES	ORIGIN Query Match Best Local S	Matches Qy 101 Db	Oy 1073

BJ296612 BJ290275 BJ262654 CK159678 CK158306

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1020 CGGCCGGGATTGGAGACACACACACAACAACAACAACGGCGCGTGAGAAATCAAC 1079
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1020 CGGGCCGGGATTGGAGACAGAGCCAAAAGCAACAAAAAGTGCGCGTGAGAAATCAAC 1079
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooldeae; Triticeae; Triticum.
1 (bases 1 to 631)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CGGCCCGGGATTGGAGACAGAGCCCACAAGACAACAACAAGAAGTGCGCGTGAGAAATCAAC 60
                                                                                                                                                                                                                                                                                        /clone lib="wpalc"
/note="Vector: pBluescript SK+; Site_1: EcoRI; Site_2:
Xho1; Wheat (Triticum aestivum) pre-meiotic anthers JIC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93, THE Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 10
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genoplante, a major partnership french program in plant genomics Unpublished (2003)
Contact: Genoplante
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l Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA Tel: 302-631-2602
Fax: 302-631-2607
Email: Scott.V.Tingey@USA.dupont.com
Seq primer: M13.
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                                                                                                                                                          /organism="Triticum aestivum"
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JOURNAL
COMMENT
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AUTHORS
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KEYWORDS
SOURCE
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CD938039
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                                                                                              CD867174 STO bp mRNA linear EST 11-JUL-2003 AZO2.105J01F001124 AZO2 Triticum aestivum cDNA clone AZO2105J01,
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Bogermatophyta; Diliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
1 (bases 1 to 594)
Tingey,S.V., Moore,G., Griffiths,S., Powell,W., Wolters,P.,
Dolan,M., Hainey,C., Maido,G., Caraher,N. and Hanafey,M.K.
Dupont Wheat cDNA Sequence in collaboration with the John Innes
                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Beprmatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
(bases 1 to 570)
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Unpublished (2003)
Contact: Genoplante
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1073 AATCAACAAGCGGTGCTTGCCGAGAAGAGAGAGAGAGAG 1111
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Pred. No. 1.4e-41;
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Contact: Scott V. Tingey
Crop Genetics
E. I. DuPont de Nemours and Company
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Triticum aestivum
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Triticum aestivum
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셤 ò 용 VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

DEFINITION

RESULT 5 CD865240

ACCESSION

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1024 CCGGGATTGGAGACAGAGCCCACAAGGCAACAACAAGTGCGCGTGAGAAATCAACAAGA 1083
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Pgermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.

    (bases 1 to 643)

                                                                                                                                                                                                                                                                                        /mol type="miniord" described."
/mol type="miniord" described.
/db xref="taxon:4565"
/dclone="wdk3c.pk008.e19"
/lab host="DH108"
/clone lib="wdk3c"
/note="voctor: pBluescript SK+; Site_1: EcoRI; Site_2: XhoI; Wheat (Triticum aestivum L.) developing kernel, 14 days after anthesis."
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Tel: 33 1 69 47 54 10
Fax: 33 1 69 47 54 10
Finis sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com
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                  Contact: Scott V. Tingey
Crop Genetics
B. I. Dubont de Nemours and Company
I. Indovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
Tel: 302-631-2602
Fax: 302-631-2607
Email: Scott.V.Tingey@USA.dupont.com
Seq primer: M13.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 7.9%; Score 88; DB 6; Length 430; Best Local Similarity 100.0%; Pred. No. 1.2e-35; Matches 88; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                         /organism="Triticum aestivum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .643
/organism="Triticum aestivum"
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/clone="F1116120"
/tissue_type="leaf one"
/clone_lib="F1"
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Triticum aestivum
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/cultivar="recital"
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Genoplante
Unpublished (2002)
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CD884411
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                                                                                                                                                                                                                   CD865240 624 bp mRNA linear EST 11-JUL-2003 AZO2.073123F000912 AZO2 Triticum aestivum cDNA clone AZO2073123,
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I (basea: I to 43)

Tingey,S V., Powell,W., Wolters,P., Dolan,M., Hainey,C., Yuan,Z., Miao,G., Caraher,N. and Hanafey,M.K.
                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae, Triticeae, Triticeae, Triticeae.
1 (bases 1 to 624)
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  1 CGGGCCGGGATTGGAGACAGAGCCCACAAGGCAACAACAAAAGTGCGCGTGAGAAATCAAC 60
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Unpublished (2003)
Contact: Genoplante
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100.0%; Pred. No. 1e-36;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
                                                1080 AAGCGGTGCTTGCCGAGAAGAGAGAGAGAGAG 1111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Triticum aestivum"
/mol_type="mRNA"
/culfivar="tecital"
/db_xref="taxon:4565"
/clone="AZO2073123"
                                                                        1082 GCGGTGCTTGCCGAGAGAGAGAGAGAGAGAG 1111
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Triticum aestivum
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/clone_lib="AZ02"
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source

FEATURES

Best Loca Matches

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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

TITLE

DEFINITION

ACCESSION

RESULT 6 CA712930 LOCUS

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Gaps

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LA/UL/48 556 bp mRNA linear EST 26-NOV-2002 wkm2c.pk005.j20 wkm2c Triticum aestivum cDNA clone wkm2c.pk005.j20 5' end, mRNA sequence.
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G118.125L08F010828 G118 Triticum aestivum cDNA clone G118125L08,
                                                                                                                                                                                                                                                                                                                                                                                             Triticum aestivum
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Pooideae, Triticeae, Triticum.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
1 (bases 1 to 556)
Tingey,S.V., Powell,W., Wolters,P., Dolan,M., Hainey,C., Yuan,Z.,
Miao,G., Caraher,N. and Hanafey,M.K.
Genoplante, a major partnership french program in plant genomics Unpublished (2003)
Contact: Genoplante
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/cultivar="recital"
/db_xref="taxon:4565"
/clone="G118125L08"
/tissue type="grain (118 degrees per day after
pollination)"
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
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5.8%; Score 64; DB 6; Le
Best Local Similarity 100.0%; Pred. No. 1.2e-22;
Matches 64; Conservative 0; Mismatches 0;
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Triticum aestivum
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/clone="WHE4351 G12_M23"
/tissue type="Whole florets with anthers"
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were grown in a glasshouse. Anther meiotic stage was
determined microscopically after removing a single anther
from a primary floret. If determined to be between (and
including) meiotic stages pre-meiosis and metaphase I,
remaining floret tissue was collected and pooled for
library construction. The tissue, toral RNA, and poly(A)
RNA were prepared, cDNA synthesised, and directionally
ligated into pSPORT1 by TIM Sutton in the P Langridge Lab
at the Department of Plant Science, University of
Adelaide, Waite Campus, Australia. Average insert size
1.4KD. Plassmid DNA preparations and DNA sequencing were
performed in the OD Anderson lab (all other authors)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
                                                                                                                                                                                                                                                                                                                                               CF132917 642 bp mRNA linear EST 24-JUL-2003 WHE4351_G12_M23ZT Wheat meiotic floret cDNA library Triticum aestivum cDNA clone WHE4351_G12_M23, mRNA sequence.
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                                                                            Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooldeae, Triticae, Triticum.

1 (bases 1 to 642)
Anderson,O.D., Chao,S., Crossman,C., Langridge,P., Lazo,G.R., Pham,J., Rausch,C.J., Sutton,T., Woo,J. and Wilson,C.
The structure and function of the expressed portion of the wheat genomes - Meiotic floret oDNA library
                                                                                                                             Gaps
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     Pred. No. 1e-23;
; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/cultivar="Chinese Spring"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Triticum aestivum (bread wheat)
Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: oandersn@pw.usda.gov
Sequences have been trimmed t
quality sequence with phred s
Seq primer: T7 primer.
Location/Qualifiers
                            ·;
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Matches 66; Conserv
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Figuration aestivum (bread wheat)

ISM Triticum aestivum (bread wheat)

ENKaryora, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticaea; Triticum.

CB (bases 1 to 422)

RS Anderson, O. A. Appels, R., Balley, P., Blake, T., Close, T., Cloutier, S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafson, P., Herrmann, R.G., Holton, T., Jacquarin, J.M., Jia, J., Joudrier, P., Langridge, P., Lazo, G.R., Lin, J.J., McGuire, P., Contier, P., Langridge, P., Lazo, G.R., Lin, J.J., McGuire, P., Sorrells, M., Warburton, M. and Wenzel, G., International Triticeae BST Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticeae

AL Unpublished (2000)

Contact: Schuch W

Zeneca Wheat Improvement Centre, Norwich Research Park
Colney Lane, Norwich NR4 7UH UNITED KINGDOM
Tel: 44 1603 250 260

Fax: 44 1603 250 699

Email: wolfgang schuch@aguk.zeneca.com
International Triticeae BST Cooperative (ITEC)

http://wheat.pw.usda.gov/genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BE419251 H3R000101 ITEC WWR Wheat Root Library Triticum aestivum CDNA
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/mol type="mRNA"
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/clone="wWR021.H3"
/tissue type="root"
/clone lib="ITEC WWR Wheat Root Library"
/note="W13 Reverse sequencing primer used for 5' end
                                                                                                    Gaps
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                                   Query Match
5.7%; Score 63; DB 6; Les
Best Local Similarity 100.0%; Pred. No. 4.2e-22;
Matches 63; Conservative 0; Mismatches 0;
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BJ257084
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1 (bases I to 637)
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                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
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/lab.host="bH108"
/clone_lib="wkm2c"
/nore="Site_l: BcoRI; Site_2: XhoI; Wheat (Triticum aestivum L.) kernel malted_175 hours at 4 C"
                                                                                           Crop Genetics
E. I. DuPont de Nemours and Company
1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
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pollination)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 5.7%; Score 63; DB 6; Length 556; Best Local Similarity 100.0%; Pred. No. 4.2e-22; Matches 63; Conservative 0; Mismatches 0; Indels
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10

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    /organism="Triticum aestivum"

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Triticum aestivum
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/cultivar="recital"
                                                                                                                                                                                                                                                                                                                 ocation/Qualifiers
   DuPont Wheat cDNA Sequence
Unpublished (2002)
Contact: Scott V. Tingey
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E 1 (bases 1 to 579)
S Ogihara, Y. and Murai, K.

E Expressed genee in Triticum aestivum
Unpublished (2002)
C Contact: Tadasu Shin-i
C Contact: Tadasu Shin-i
C Contact: For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Trel: 81-559-81-6855
Email: tahini@genes.nig.ac.jp.
                                                                                                                                                                                     Enkaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Enkaryota; Viridiplantae; Streptophyta; Enkaryota; Viridiplantae; Streptophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticae; Triticum.

E pooideae; Triticae; Triticum.

S Ogihara, Y. and Murai, K.

Expressed genes in Triticum aestivum
Upublished (2002)

C Ontear: Tradeau Shini Center of Genetice
Institute of Genetice
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BJ221033 Y. Ogihara unpublished cDNA library, Wh Triticum aestivum
BJ221033
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100.0%; Pred. No. 1.5e-21;
iive 0; Mismatches 0; Indels
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/mol type="mRWA"
/oulfivar="Chinese Spring"
/db xref="taxon:4565"
/clone="whh19m06"
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Triticum aestivum
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Triticum aestivum
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Location/Qualifiers
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae; Triticae; Resource Information

AL Unpublished (2002)

AL Unpublished (2002)

National Institute of Genetics

1111 Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6855

Fax: 81-559-81-6855

Email: tshini@genes.nig.ac.jp.
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/clone="wh22013"
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/dev stage="Feekkes' scale 9"
/clone_lib="Y. Ogihara unpublished cDNA library, Wh"
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BJ253061 Y. Ogihara unpublished cDNA library, Wh_f Triticum aestivum cDNA clone whf27c17 3', mRNA sequence.
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Best Local Similarity 100.0%; Pred. No. 1.8e-20;
Matches 60; Conservative 0; Mismatches 0;
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/clone="whf27c17"
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Job time : 4255 secs
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae; Triticaea; Promoter of thioradoxine TaTrxh2 in wheat Promoter of thioradoxine TaTrxh2 in wheat Dancter of thioradoxine TaTrxh2 in wheat Dancter of thioradoxine Common wheat)

No Triticum aestivum (common wheat)

PD 24-DEC-2002

PF 17-MAY-2000 JP 2000618471

PR 17-MAY-1999 FR 99/06231
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5/09,A01H5/00,C12N5/10//(C12N5/10,C12R1:91),C12N15/00,
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/db_xref="taxon:4565"
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JP 2002543844-A/2.
Triticum aestivum (bread wheat)
Triticum aestivum
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5.1 152294
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5.0 142752
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AC079853 Oryza sat
AC091787 Oryza sat
AC137618 Oryza sat
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AC135927 Oryza sat
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PP 17-MAY-2000 JP 200618471

PR 17-MAY-1999 FR 99/06231

PI MARIE FRANCOISE GAUTIER; TANIA IHORAI, PHILIPPE JOUDRIER PC CLANIS,09,A01185/00, CL2NS/10//(CL2NS/10,CL2NIS)10, CL2NIS/00, PC
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CAGCCAGTTTATTATATAAACAGGCTATATAGCTGACCTGGCAGTGCTATAGAGCCGGCA
                                                     AAACAACAAATCCGGGCGTTCAGCAAGTCGGAATGAATTTCGGCTCATCACTCATTGTCG
                                                                                         TGGGCCTCACGCGTATTCGCCTAACCGTGTTTGAATCAGACCCTCACGAAGCCACGGCTC
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/organism="Triticum aestivum"
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/db_xref="taxon:4565"
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Matches 1111; Conservative
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Oy 421 AGAAAGAAAGTAGGAGTGAGAAGGGGGTTGGCTTCGTCAATCGCTAGCGACAA 480 nh 421 AGAAAGAAATTGAAATTGAAAAAGAGGTTCGGGGTTCGTCAATCGCTAGAAAA 480	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	541 ATCAGTATGCCTTTCTTCTTCTTCATGCAAGCATTAAATACTATAGCTAATCTA	Qy 601 CAGCCAGTTATTATATAACAGGCTATATAGCTGACCAGGCAGTGCTATAGAGCCGGCA 660	Db 721 AAACAACAAATCGGGGCGTTCAGCAAATCGGAATTGGGCTCATCATTGTCG 780	901 901 961	Oy 1021 GGGCCGGGATTGGAGCCCACAAGGCAACAAAGTGCGCGTGAGAAATCAACA 1080 1021 GGGCGGGATTGGAGACCCACAAGGCAACAAAGTGCGCGTGAGAAATCAACA 1080 Qy 1081 AGCGGTGCTTGCCGACAAGAGAGAGAGAGAG 1111 Db 1081 AGCGTGCTTGCCGAGAAGAGAGAGAGAG 1111	RESULT 5 AP005428 LOCUS AP005428 LOCUS DEFINITION Organ sativa (japonica cultivar-group) genomic DNA, chromosome 2, PAC clone:P0693E08. ACCESSION AP005428 VERSION AP005428 GI:45382012	_	REFERENCE 1 TUTURS Sasaki,T., Matsumoto,T. and Katayose,Y. TITLE Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2, PAC TITLE Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2, PAC TITLE Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2, PAC Clone:POGSTB108 JOURNAL Published Only in Database (2002) REFERENCE 2 (bases 1 to 157969) AUTHORS Sasaki,T. Matsumoto,T. and Katayose,Y. TITLE Direct Submission JOURNAL Submitted (12-JUN-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai
QY 961 TAGGGGGGATAATTCTGATTCCTGCCTGCCGGACAATTTATCTTTGGGGAGGC 1020	QY 1021 GGGCCGGGATTGGAGACAGAGCCACAAGGCAACAAAGTGCGCGTGAGAAATCAACA 1080 	Qy 1081 ACCGTGCTTGCCGAGAAGAGAGAGAG 1111 	RESULT 4 AX047681 LOCUS LOCUS LOCUS LOCUS LOCUS REFINITION Sequence 1 from Patent W00070065. ACCESSION AX047681.1 GI:11876716 KEYWONDS SOURCE Triticum aestivum (bread wheat) REWANDS FILLICUM aestivum (bread wheat) REWANDS FILLICUM aestivum (bread wheat) REWANDS	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; REFERENCE 1 AUTHORS Gautier,M.F., Ihorai,T. and Joudrier,P. TITLE Promoter of thioredoxine tatrxhb in wheat JOURNAL Patent: WO 0070065-A 1 23-NOV-2000; FRATURES 1. Cocation/Qualiflers FRATURES 1. DARY 2000/AUTHORAIDE LA RECHERCHE AGRONOMIQUE (INRA) (FR)	xon 112. xon 122. xon 233. xon 224. xon	OKIGIN Query Match Query Match Best Local Similarity 100.0%; Score 1111; DB 6; Length 2687; Best Local Similarity 100.0%; Pred. No. 0; Matches 1111; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy	Oy 61 AGACGAGGGGCGATGTGCCTGTTCCTTGGCGAGGCGTTTGGCAGCCGCCGC 120	Oy 181 TTTATGGCGATGGCGTTAGCGGTCTTGGGGGGTCTTGGGGGGGTACATTTGAAGATGTG 240	Db 241

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/noce="supported by full-length cDNA(s): AK067325"
join(7629. 8090,11440. .11508,11600. .11668,12554. .12640,
13245. .1312,13410. .13551)
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/note="contains full-length cDNA(s): AK067325"
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EWLSVTTDDAKTVLAAIAISLAFRSFVAEPRFIPSLSMFPTFDVGDRIVAEKVTYYFR
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PCMKKGGVRFTINGHDYFQLVILITNVQAAGSIKAMDVKGSKSPDWMAANAHNWGAQWHS
                                                                                                                                                                                                                                                                                                                                                                                                                                            KPCINDIVIFKSPPVLQEVGYTDNDVFIKRIVAREGDVVEVHKGKLVVNGEVRBEFI
LEPPSYDMNPVQVPENSVFVMGDNRNNSYDSHVWGPLPSKNILGRSIFRYWPPGRIGS
TTTDCLIPETNPSSLIDVKLAK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="hypothetical ORF
predicted by GENSCAN
this category is not included in IRGSP standard"
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join(15268. 15743,16184. 16496)
gene="P0693E08.4"
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join(18903. .19081,21594. .21603)
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complement (join (17966. .18049,18114. .18212))
/gene="Po699808.5"
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/gene="Po699808.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |oin(<15268. .15743,16184. .>16496)
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                   13245. .13312,13410. .13886)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15268. .16496
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2-1-2, TBukuba, IDaraki 305-8602, Japan
(E-mail:tesaskiemisa affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-741, Fax:81-298-38-7468)

On Mar 11, 2004 this sequence version replaced gi:21396538.
Genes were predicted from the integrated results of the following: Gens were predicted from the integrated results of the following: GENSCAN (http://ccR-081.mit.edu/GenSM2K/N.mtml), FGENESH
(http://www.igfrc.org/tdb/glimmerm/glmr.form.html), FGENESH
(http://rgp.dna.affrc.go.jp/RiceHWM/), SplicePredictor
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(http://rgp.dna.affrc.go.jp/RiceHWM/), SplicePredictor
(http://rgp.dna.affrc.go.jp/RiceHWM/), SplicePredictor
(http://rgp.dna.tigr.org/software/glimmerm/), BLASTN and BLASTN. The
genomic sequence was searched against NCBI NonRedundant Protein
database, nr (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA
sequence database at RGP or DDBJ. Protein homologise of the coding
regions were searched against NCBI NonRedundant Protein database
with BLASTN with the corresponding DDBJ accession no. and RGP clone ID.
Pull-length cDNAs represent the identified cDNA sequences using
BLASTN with the corresponding DDBJ accession no.
A gene with identity or sugainst DDBJ accession no.
A gene with identity or protein name to indicate the homology level
such as same name, 'putative-' and 'like protein. A gene without
significant homology to any protein but with full-length of partial
sequence) is classified as an 'unknown' protein. A gene predicted
by two or more gene prediction program is also classified as
'hypothetical' protein according to IRGSP standard. A gene
predicted by a single gene prediction program is also classified as
'hypothetical' protein according to IRGSP standard. A gene
predicted by a single gene prediction program is also classified as
'hypothetical' protein according to IRGSP standard.
This sequence of P0693B08 clone has an overlap with P0005C08 (DDBJ
RDGGCB ADGGCB A
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/gene="P0693E08.3"
join(7496. .8090,11440. .11508,11600. .11668,12554. .12640,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             translation="MWQWSCCRRLLPVVCGIGDLTAGTGAGRRGGRKRPPTAYLPNKY"
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non-coding transcript
probably inactive due to including stop codon(s) in CDS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"
/cultivar="Nipponbare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="supported by full-length cDNA(s): AK106502"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(1878, 2063)
/gene="P0693E08.1"
complement(<1878, .>2063)
/gene="P0693E08.1"
/gene="P0693E08.1"
complement(1878, .2063)
/gene="P0693E08.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://rgp.dna.affrc.go.jp/GenomeSeq.html.
Location/Qualifiers
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/protein_id="BAD28618.1"
/db_xref="GI:502514?9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'db_xref="taxon:39947"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <4350. .>5856
/gene="P0693E08.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RLRVEYTWRRTPNGRGW"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="P0693E08.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="P0693E08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .5856
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                                                                                                        COMMENT
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/product="thioredoxin h"
/product="thioredoxin h"
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/db_xref="TOA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1019 GCGGGCCGGGATTGGAGACAGAGCCCACAAGGCAACAACAAGTGCGCGTGAGAATCAA 1078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Serrato, A.J., Crespo, J.L., Florencio, F.J. and Cejudo, F.J. Characterization of two thioredoxins h with predominant localization in the nucleus of aleurone and scutellum cells of germinating wheat seeds
Plant Mol. Biol. 46 (3), 361-371 (2001)
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                                                                                                                                                                                                                                                                                                                     Legido, F.J.

Cejudo, F.J.

Direct Submission

Submitted (06-JUL-2000) Cejudo F.J., Instituto de Bioquimica
Submitted (06-JUL-2000) Cejudo F.J., Instituto de Bioquimica
Vegetal y Fotosintesis, Universidad de Sevilla, Avda Americo
Vespucio s/n, 41092-Sevilla, SPAIN

Location/Qualifiers
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1; Poales; Poaceae;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sasaki,T., Matsumoto,T. and Katayose,Y.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 8, clone:P0562A06
Published only in Database (2002)
2 (bases 1 to 154198)
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Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyte; Em
Spermatophyta; Magnoliophyta; Liliopsida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.2%; Score 68.6; DB 8; 91.4%; Pred. No. 5.4e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue type="aleurone"
/dev stage="germinating seed"
/country="Spain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .629
/organism="Triticum aestivum"
/mol type="mRNA"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
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/note="ORF"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
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CDS
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AUTHORS
TITLE
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REFERENCE
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TITLE
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PUBMED
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AUTHORS
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JOURNAL
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                                                                       REFERENCE
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SOURCE
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AP005524
                                                                                                                                                                                                                                JOURNAL
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                                                                                                                                                                                                                                                                                           .30051,30102. .30302,30471. .30527,
                                                                                                                                                                                                                                                                                                                                                                                      /note="start and end point are not identified"
join (2921). .29733.29771. .30051,30102. .30302,30471. .30527,
31173. .31237,31417. .31638)
/gene="p0693E08.9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102959 ATCAGGTGCACATGTGAATATTAAAT-----ATCTAAATCTTCGATAGAGATAAACAA 103011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            102782 TTAGAGCAGGATTAATAGATCCTAGTCAGCCGGCGCTAGCATGTTACCCGTCAGCGAAAT 102841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             102900 -CCGGCTGAAGCGCAACACATGAAGAAAAAAATGATTTCTTCCAATCAGATGCGAGGAG 102958
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                                                                                                    IWCPDYQQVWKRLGDADSDERACAVAYHDGAAVCVDLARCYVHEIGGPAAGDQTTFLP
PEDBEGKYRRSKYLLELRGELLLASYLDAGAGCHDDDDDDDDDDDDBLSLSVYAFDLVAALN
ALDQLDAAVDGAGOPPSPS SWEKWDGATGDHVLFLGYPRS FAVEARYGGSVPGGS
AYFVGRSKPCRVYRCSFEDDGTAATLVDTLPAGWNDERCWWFLPEPDIAPVIGART"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MYSYSDLPPELVCLIGRRLHTAINVVRFHAVCSDWRQSLRHIPP
SPPPAAALLDWLPAPSSGDDADAAGVACRCVFSKTSYHAPGLCFRDRRVAHADGTAS
WFINDKLVNPLTGWINVGRVKKYPWMWTDGSKGFFHCVVSGDGSLLVYRLSPRWRSPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RLSVSVHAFDVDAAVHALDPDAAEPPVAARQRRRWWKRCPPDGTTREEQEEDAAARA
YQQRRQHQQRDLRIHVSDLSPQVDSCRLREMYSEHGKVVVRAGEGRVRQAGGDREGLGW
LAVGCNLIPVGQILLPTRFPNRHYEDGIDEDSKVTGIFEEDLPGELLPMPDPSWERPL
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                                       RPSFLPWLLAPWPTPDDDTAAAGGACRCVFSRTTYHAPGLGIRDKRVAHYDGGASWFV
GGLFVNPLTGRAAACAVDDPYLSDWIDNEGSRCIFSGDGTLLTCCFYDAGPPLSIYGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RISITPTTAAPPATVLASPHAPMPLPDEPRKVRRHSYLLELRGELLLASVLQDDDDDD
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thioredoxin H.
Triticum aestivum (bread wheat)
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             translation="MTLISDLPPELLPCIAGHLHAAVDVVRFHAVCREWRDALRYLPR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      408 CITAAACTGGAGGAGAAAGAAGTAGGAGTGAGAAGGGCGTCGCCGCTTCGTCAATCGCT 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              348 TIAGAGCAAGIAIAAIAAGICCIAGICAGCIGGCIAIAAGAIGIICCACAICAGCAAAIC 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               468 AGCGATAGCACAAGCTCCCATGGAATCGAGCCAACATGCAACCGCCACAATGACTAAAGG 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           588 TATAGCTAATCTACAGCCAGTTTATTATATAAACAGGCTATATAGCTGACCTGGCAGTGC 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KPHPLREPSPTPHPPASDAVAHAATDTAGSIFACCHYRLSRSKGKGAEEERRRG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 157969;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TATAGAGCCGGCAGCAGGCTATGTTATTAACATTGCTCTTAT 103113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 71.2; DB 8; Length 19
Pred. No. 2.2e-10;
0; Mismatches 138; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TATAGAGCCGGCAGCCGGCTCTTCTATTAGCTTTGCTCTTAT 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    join(<32993. .33468,33578. .>33890)
/gene="P0693E08.10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="predicted by FGENESH etc."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAB404845 629 bp mRNA Triticum aestivum mRNA for thioredoxin h. AJ404845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="hypothetical protein"
/protein_id="BAD28623.1"
/db_xref="G1:50251484"
                                                                                                                                                                                                                                                                                        join(<29219. .29733,29771. .3
31173. .31237,31417. .>31638)
/gene="P0693E08.9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32993. .33890
/gene="P0693E08.10"
                                                                                                                                                                                                                                29219. .31638
/gene="P0693E08.9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      codon start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 56.7%;
Matches 194; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             103072
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VERSION
KEYWORDS
SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
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EMVAVLDLDVLFYPCPKNGPTFŘPKVLEMGGKQPFYMYDPNTGVAMYESDAIIKYLA
KYCOGTVPIMLSLGILTTITAGLANGGRSGKGSKYTPAKLPPEDIELWAYEGSPFCK
IVRETLYELELPHLLHSCARGSPRRQEFLKKYGIFQAPYIEDPNTGVKMFESADIIDY
LRATYAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tränslation="MDSSFSPAPASRGRWSWGSALVGAASTAAAAAVLLCRPRDPTFE
LISISLSTFRERPAALDIGITUTUHATUPNVPVRYGPSTVSILYDGAHLGTARLDA
GROPPTSCRLLHLDRAKLDAVELAHHARSILADTARRHWELDAVKIAGEAAVALWSRR
FSVSIDSHIVVDPVFLDVIEQENHSEWOLYLT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translation="MAATALHLPPLLLARRLRFSSAAASTSTSRRTTRLSAQLDDTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASTSTSTSDKPAAASSFAPPDFKPPEPKTFEVKPGQSDDIVTASLAIPFRLGTGVFA
LGYSVSLVSPDEVAPDEYALDFQGRKVKESSKIGQCPRPEKPIEIYEFEGCPFCRKVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (join (26564. .26981, 27068. .27130, 27982. .28102,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /noce="supported by full-length cDNA(s): AK069761"
join(8549. .8859,8978. .9042,9255. .933,9484. .9502,
9583. .9702,10049. .10118,10201. .10244,10410. .10451,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probably inactive due to including stop codon(s) in CDS" complement(22111, .25642) /gene="P0562A06.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06555. .10584.10680. .10747,10905. .10962,11040. .11409)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="contains EST(s): AU173424(R3033),AU173425(R3033)
contains full-length cDNA(s): AK069761"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(12959. .19068)
/gene="P0562A06.6"
/note="contains full-length cDNA(s): AK071334,AK060581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    join(8510. .8859,8978. .9042,9255. .9333,9484. .9502,
9583. .9702,10049. .10118,10201. .10244,10410. .10451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="similar to Arabidopsis thaliana chromosome 3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="probably inactive due to 5' exon missing in
pseudogene, RNA-directed DNA polymerase"
                                                                                                                                                                                                        this category is not included in IRGSP standard"
join(6892. 6993,7148. 7184,7470. 7579)
/gene="P0562A06.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         this category is not included in IRGSP standard"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="start and end point are not identified"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           product="putative auxin-regulated protein"
protein_id="BAD13127.1"
db_xref="GI:45736096"
                Join (5570. .5640,6229. .6318,6443. .6557)
                                                                                                                                                                                                                                                                                                                           join(6892. .6993,7148. .7184,7470. .7579)
/gene="P0562A06.3"
      KGLTEKFKEKDTRYSGSATLSYDGFLSMVIPFIVP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon start=1
/product="hypothetical protein"
/protein_id="BAD13128.1"
/db_xref="G1:45736097"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (22111. .25642)
/gene="P0562A06.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (26564. .29230)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(12959. .19068)
/gene="P0562A06.6"
                                                                                                                                                                                                                                                                                                                                                                                        /note="hypothetical ORF
predicted by GENSCAN
                                                                                           Join (5570. .5640,6229.
                                                                                                                                                            /note="hypothetical ORF predicted by GENSCAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     non-coding transcript
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="P0562A06.5"
<12290. .>12868
/gene="P0562A06.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3510. .11409
/gene="P0562A06.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12290. .12868
/gene="P0562A06.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'gene="P0562A06.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12290. .12868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        190024"
                                                                                                     misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
                AL Submission

AL Submission

Algrothylogical Sciences, Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Inbaraki 305-8662, Japan

Agrobiological Sciences, Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Inbaraki 305-8662, Japan

(B-mail: teasasakiamias afferc.go.jp, URL:http://rgp.dna.afferc.go.jp/, URL:http://rgp.dna.afferc.go.jp/, URL:http://rgp.dna.afferc.go.jp/, URL:http://rgp.dna.afferc.go.jp/, URL:http://rgp.dna.afferc.go.jp/, URL:http://rgp.dna.afferc.go.jp/RiceHMM/, RGENESH

(http://www.softberry.com/), GeneWark.hmm

(http://www.softberry.com/), GeneWark.hmm

(http://www.softberry.com/), GeneWark.hmm

(http://www.idgr.org/dbb/glimmerm/glim_form.html), RiceHMM

(http://globin.cse.puu.edu/html/docs/eim4.html), gap2

Englishase.

A gene with identity or significant homology to a protein in a same meme. '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The orientation of the sequence is from 17 to SP6 of the PAC clone. This sequence of P0562A06 clone has an overlap with OJ1150 Al1 (DDBJ: AP003928) clone at 5' end and with P0604E01 (DDBJ: AP065544) clone at 3' end. Detailed information on overlap and assembly quality together with annotation of this entry is available at http://rgp.dna.affrc.go.jp/GenomeSeq.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HGGGGYPSSTYPPPPSSSQAYPMGMGGFLVFPPGTHPDVERAFRAVDRDGSGSIDER
ELQDALSSAYHRFSIRTVRLLLFLFNKPASHSPSRMGPAEFVSLMNCLGQWRGIFDRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation="MADYNRYGYGGYGSTPSAPPASSYGYTTTPSAPPASSSSYGYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DRDGSGKIEKDELREALRSLGYAVPPSVLELLIANYNNGVSSRGALDFDNFVECGMIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="supported by full-length cDNA(s): AK099458"

complement(join(2422. .2526,2641. .2659,2763. .2938,

3417. .3463,4103. .4517)}

/gene="P0562A06.1"

/note="contains EST(s): AU068303(C12982),AU068304(C12982)

contains full-length cDNA(s): AK065151,AK099458"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="supported by full-length cDNA(s): AK065151"
complement(join(2133. .2526,2641. .2659,2763. .2938,
3417. .3463,4103. .4572))
/gene="P0562A06.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"
/cultivar="Nipponbare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="putative fiber protein Fb1"
/protein id="BAD13126.1"
/db_xref="G1:45736095"
   Sasaki, T., Matsumoto, T. and Katayose, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3417. .3463,4103. .4572))
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/gene="P0562A06.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     db_xref="taxon:39947"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (join (2126.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /chromosome="8"
/clone="P0562A06"
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/clone="P0604E01"
47. .821
                                                                                                AP005544.3 GI:42409221
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AUTHORS
                                                                      ACCESSION
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                                                                                                                        KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119860 CTTATAGCCAACCTCTACGCCAGTTTACTATATGCACTGGCTTTCTCAAATGCTTAAAGT 119919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119628 GCTAAGAGCAAGTATAGTGAAGCACAGTCAGCCGGCGAAATAACTTACCACGTCACCCCAA 119687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119688 ATCTGAGGTGGAAAGAGAGAGAAATCCTAATAGAGAATAGGACGGGCGATTGGTGAGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119748 CTCGCTTGAAG-----CAGCAGAACCGAGATAAAAAGCTTCTTCTCAGCCTGCTGCTGCA 119799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119920 GACATGGCCACCTTATTGCGCCAGCTGCCGGTGAAACCATTAACCATGCTCTAATCGTCA 119979
                                                                                                                                                                                                                                                                                                                                                                          /procein_id="BAD13129.1"
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TEVKGIMMDNIEKILERGEKIELLVGKTETLQSQADSFHRHGREIRRKWMLQNLRFKL
MVGGAVAALILFLWLICGGFKC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  465
                                                                                                                                                                                                                                                                                                                              /product="putative vesicle-associated membrane protein 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="supported by full-length cDNA(s): AK103638"
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33145. .33187)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             466 CTAGCGATAGCACAAGCTCCCATGGAATCGAGCCAACATGCAACCCGCACAATGACTAAA 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   526 GGCAAACGCCAGCCAAICAGIAIGCCTIICICTGCAICTITCTTCAIGCAAGCAITAAAI 585
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(join(29750, .30219,30364, .30625,31510, .31599,
33145, .33273))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similar to Arabidopsis thaliana chromosome 3, NP 566962"
                                                                                                                                                                                                                                                /note="contains EST(s): AU100788(C50778), C97037(C50778)
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contains full-length cDNA(s): AK103638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 586 ACTATAGCTAATCTACA-GCCAGTTTATTATATAAACAGGCTATAT-----AGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GACCTGGCAGTGCTATAGAGCCGGCAGCCGGCTCTTCTATTAGCTTTTGCTCTTATGGCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            346 GTTTAGAGCAAGTATAATAAGTCCTAGTCAGCTGGCTATAAGATGTTCCACATCAGCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 154198;
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28202. .28403,28511. .28759,29097. .29230))
gene="P0562A06.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 65.2; DB 8; Length 15
Pred. No. 1.9e-08;
0; Mismatches 153; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="unknown protein"
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Matches 206; C
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Direct Submission

Direct Submission

Direct Submission

Submitted (18-JUL-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tankubai, Ibaraki 305-8602, Japan

(B-mail:teasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-18-7468)

On Feb 4, 2004 this sequence version replaced gi:34740254.

Genes were predicted from the integrated results of the following: GENSCAN (http://www.softberry.com/), GeneMark.html), FGENESH

(http://www.softberry.com/), GeneMark.html), FGENESH

(http://www.tigr.org/tdb/glimmerm/glmr.form.html), RiceHWM

(http://globin.cse.psu.edu/html/docs/sim4.html), gap2

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(http://globin.cse.psu.edu/html/docs/sim4.html), gap3

BLASTN with the corresponding DDBJ accession no. and RGP clone ID

Rull-length cDNAs represent the identified CDNA sequences using

BLASTN with the corresponding DDBJ accession no.

A gene with identi
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                                         PLN 24-MAR-2004
                                                                                                                                                                                                                                                                                                          Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantes; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone
APU05544 159049 bp DNA linear PLN 24-MAR-20
Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 8,
PAC clone:P0604E01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The orientation of the sequence is from SP6 to T7 of the PAC clor This sequence of po604801 clone has an overlap with P0562A06 (DDB AP06524) clone at 5' end and with P0543D10 (DDBJ: AP004587) clor at 3' end. Detailed information on overlap and assembly quality
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/cultivar="Nipponbare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAC
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join(<47. .148,395. .474,569. .>821)

/gene="P0604E01.1"

join(47. .148,395. .474,569. .821)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sasaki,T., Matgumoto,T. and Katayose,Y.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 8,
clone:P0604E01
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sasaki,T., Matsumoto,T. and Katayose,Y.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Published Only in Database (2002)
2 (bases 1 to 159049)
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/chromosome="8"
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39751 CTCGCTTGAAG-----CAGCAGAACCGAGATAAAAAGCTTCTTCTCAGCCTGCTGCA 39802
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(join(<36723. .36837,37482. .37651,38018. .38287,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="XS domain containing protein-like"
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/bc.xref="GI:45736158"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /trānslation="MAIVDLVNAGEQQQMGSKRAAAEDGDGGVDDSREYYCRRGVRHL
CDSGITRLPGNYVLPASDRPGQAAGAAAAGGSVKLPVVDLSRLRVPSERGAVLRTLD
AACREYGFFQVVNHGVGGEVVGGMLDVARRFFELPQPERERYMSADVRAPVRYGTSFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QVRDAVLCWRDFLKLACMPLAAVVESWPTSPADLREVASRYAEANORVFMEVMEAALE
AGVGGGGGWWWEDLAAGTQWMTWNCYPECPECPPELTICAMPDHYDYGFLTLVLQDEVVAGLQ
VMRAGEWLTVDPLAGSVVXVQDPLEILSNGRYRSVLARVKVNSRELRVSVASFHSVA
PERVVSPAPELIDDRHPRRYMDTDLATFLAYLASAAGNHKSFLHSRRLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ų.
                                     /gene="P0604E01.5"
/note="putative GAG-POL precursor"
complement(join(23389. .24084,24131. .24744,24910. .25226,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 465
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                                                                                                                                                                                                                   .24084,24131. .24744,24910. .25226,
                                                                                                                                                                                                                                             /gene="p0604601.6"
/note="putative gypsy-type retrotransposon RIRE2 protein"
27168. 28265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTAGCGATAGCACAAGCTCCCATGGAATCGAGCCAACATGCAACCGCACAATGACTAAA 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="supported by full-length cDNA(8): AKI07117"
join(33466. .34525,34906. .35833)
/gene="b0604E01.8"
/note="supported by full-length cDNA(8): AKI07230"
join(33620. .34525,34906. .35151)
/gene="p0604E01.8"
/note="contains full-length cDNA(8): AKI07117,AKI07230"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 406 TCCTTAAACTGGAGAGAAAGAAAGTAGGAGTGAGAAGGGCGTCGGCGCTTCGTCAATCG
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/protein id="BAD13205.1"
db_xref="GI:45736159"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19;
                                                                                                                                                                                                                                                                                                                                                                                                                                /note="3' terminal repeat"
/rpt type=terminal
complement (28726. .31065)
/gene="p0604E01.7"
complement (join(<28726. .28937,31056. .>31065))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 159049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="start and end point are not identified"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (join (28726. .28937,31056. .31065))
/gene="P0604E01.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 5.9%; Score 65.2; DB 8; Length 1: Best Local Similarity 54.5%; Pred. No. 1.9e-08; Matches 206; Conservative 0; Mismatches 153; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            join(33462, .34525,34906, .35263)
.20154,20581. .22746)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (36723. .40632)
/gene="P0604E01.9"
                                                                                                                                                25638. .26587))
/gene="P0604E01.6"
complement(join(23389.
25638. .26587))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33462. .35833
/gene="P0604E01.8"
                                                                                                                                                                                                                                                                                                                                                                                           /gene="P0604E01.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40504. .>40632))
/gene="P0604E01.9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene="P0604E01.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                codon start=
       misc_feature
                                                                                                                                                                                                                   misc feature
                                                                                                                                                                                                                                                                                                                                                                 repeat_unit
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join (431). . 4488,4773. . 4807,5437. . 5625,6278. . 6457,6785. . 6969,7088. . 7183,7383. . 7428,7549. . 7655,8388. . 8489,8575. . 10211)

/gene="P0604E01.3"

/gene="pupperted by full-length cDNA(8): AK065627"

join (4368. . 4438,4773. . 4807,5437. . 5625,6278. . 6457,6785. . 6969,7088. . 7183,7383. . 7428,7549. . 7655,8388. . 8489,8575. . 9369,7088. . 7183,7383. . 7428,7549. . 7655,8388. . 8489,8575. . 9369,7088. . 7883,7883. . 7428,7883. . 8489,8775. . 9369,7088. . 7883,7883. . 7883,7883. . 7883,7883. . 7883,7883. . 7883,7883. . 7883,7883. . 7883,7883. . 7883,7883. . 7883,7883. . 7883,7883. . 7883,7883. . 7883,7883. . 7883,7883. . 7883,7883. . 7883,7883. . 7883,7883. . 7883,7883. . 7883,7883. . 7883,7883. . 7883,7883. . 7883,7883. . 7883,7883. . 78833,7883. . 78833,78833. . 78833,78833. . 78833,78833. . 78833,78833. . 78833,78833. . 78833,78833. . 78833,78833. . 78833,78833. . 78833,78833. . 78833,78833. . 78833,78833. . 78833,78833. . 78833,78833. . 78833,78833. . 78833,78833. . 78833,78833. . 78833,78833. . 78833,78833. . 78833,78833. . 78833,78833. . 78833,78833. . 78833,78833. . 78833,78833. . 78833,78833. . 78833,78833. . 78833,78833. . 78833,78833. . 78833,78833. . 78833,78833. . 78833,78833. . 78833,78833. . 78833,78833. . 78833,78833,78833. . 78833,78833,78833. . 78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,78833,7
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DDQRGGLKTLASQAHHTHELAKEVQINFSGYWEMQRKEEKRRFGSMISSLKKENQDIRS
MLKIAVTEKEAAENRLCVLKGDKDQGRSAILQIBAKGLHKVRGFGFINDUTGESEREE
NMSSNSATEISTTGRESDQQVDSLFSVVGFWENMQNEINDLRQALHKSRSDCDRLQL
LAAEQAQKIVKYELHIKOLEEREIFLLHSVTEKGLMPLPAMLKYEELTVDLKEVERA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
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/product="unknown_protein"
/protein_id="BAD13203.1"
/db_xref="d1:49736157"
/translation="MAAAASPPVPSKVDASSRPDRSPRPOSLEISWDSQAALCKRAES
CELEARVPSINPTLEPYLEDLISLYBIRPREDDYEQRHIMIDDYRKIAEETYGKK
GFPVVEARGSTMDLTASPLINDLISLYBINDERSPROKISVIRNLAKVLYAHQRN
GRCHGVLPVVTAKVPVALKVIDKGTGYBCDISVENKDGMSRSMIPKLISSIDERFQILC
YLAKFWARKAHDVNCPRDRTMSSMAIISLVAFHLQTRRPPILPAFSALLKDGPDFPSIQ
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                                                                                                                                                                                                            /translation="MATEQPSEKKPPASGGEKKAPLPKVVTLNKALKLAQTWVDKMSA
SDQDEPKAKDFEGRPPGLGLGAKVAPNVKRAAPTDPVERRLLGKVNAQKRKATEEEKT
IAQEVNDDSDDDSGETESRTSAFSKKRTAPSVTAMPLGKKAR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ARWREACELEVEAGKDAIKQINQELGPPQVALLITEELRRVKADLEAANSKLQIKEKLA
ATANAAQAADECLKLADSRSAGLQIRIEELTKQIEGEDEHAGKERGSAHRRTRYACW
PLRRLRVISASSARKWFVDQNGRLPPGTEALLQIRI"
1311. 10211
/gene="P0604E01.3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .2539,
                                                                                                                                                                                                                                                                                                 complement (1555. 3571)
/gene="P0604E01.2"
complement (join(<1555. .1944,2225. .2383,2428.
2655. .2731,3020. .>3571))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    join(19081. .20154,20581. .22746,27168. .28265)
/gene="P0604E01.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="start and end point are not identified" complement (join(1555...1944,2225...2383,2428...2655...2731,3020...3571))
/gene="P0604E01.2"
/codon start=1
/product="myosin heavy chain -related-like"
                                     'note="predicted by FGENESH etc."
                                                                                                    /product="hypothetical protein"
/protein id="BAD13201.1"
/db xref="G1:45736155"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat"
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/db_xref="GI:45736156"
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17248. .19014
/gene="P0604E01.4"
17248. .19014
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/gene="P0604E01.5"
15408. .16504
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/note="5' terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene="P0604E01.4"
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                                                                                                                                                                                                                                                                                                                                                                                              mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene
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complement (join (218798. .18812,19315. .19400,20366. .20498, 20564. .20641,21430. .21516,22464. .22554,22638. .22788, 22867. .23556,23704. .>24120))
/gene="po478802.2"
/note="start and end point are not identified"
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/product="hypothetical protein"
/protein_id="BAC79182.1"
/db_xref="Gi:32526659"
/db_xref="Gi:325269"
/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALIAEFMATLIFLYVSIATVIGYKNQRATVDACTGVGYLGVAMSFGATIFVLVYCTGG
VGGGHINPATULGIFFGRKASLYRTYLVVAQCLGALAGAGIYKGIMKRPYDALGGGA
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LATIPITGTGINPARSLGAAVLYNQHAAWKDHMIFWVGPVIGAFLAAAYHKLVLRGEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30073. .31046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="P0478E02.2"
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similar to Oryza sativa chromosome 3, OSJNBa0011L14.12"
                                                                                     (japonica cultivar-group) "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'product="putative water stress induced tonoplast
                                                                                                                                                                                                                                                                                                             /cincumce="po478B02"
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'note="predicted by FGENESH etc."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (33057. .33728)
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|cultivar="Nipponbare"
                                                                                                                                                                                                                                 'db_xref="taxon:39947"
ocation/Qualifiers
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Direct Submission

Direct Submission

Direct Submission

Direct Submission

Pelotas, Centro de Genomica e Fitomelhoramento department

Pelotas, Rio Grande do Sul 96010900, Brasil

(E-mail:acostol@terra.com.br,

URL:http://www.ufpel.tche.br/faem/fitotecnia/fitomelhoramento/,

Tel:55-53-275-7263, Fax:55-32759031)

On or before Jul 3, 2003 this sequence version replaced

gi:3017226, gi:3017227, gi:3017228, gi:3017223,

Genes were predicted from the integrated results of the following:

(http://www.softberry.com/), GeneMark.hmm

(http://opal.biology.gatech edu/GenEMark/), GlimmerM

(http://yepal.biology.gatech edu/GenEMark/), SplicePredictor

(http://rgp.dma.affr.go.jp/RiceHWM/), SplicePredictor

(http://rgp.dma.affr.go.jp/RiceHWM/)

(http://rgp.dma.affr.go.jp/RiceHWM/), SplicePredictor

(http://rgp.dma.affr.go.jp/RiceHWM/)

(http://rgp.dma.affr.go.jp/RiceHWM/)

(http://rgp.dma.affr.go.jp/RiceHWM/)

(http://rgp.dma.af
39803 TGCGACTGAGCCTGCAGCTCCTTTTCTCCCATTTGCTACTACTACATGCAAGCATTAACT 39862
                                                                                                                                            39863 CITATAGCCAACTCTACGCCAGITIACTATATGCACTGGCTTTCTCAAATGCTTAAAGT 39922
                                                                                                                                                                                                                                                                                                                                                                              39923 GACATGGCCACCTTATTGCGCCCAGCTGCAAACCATTAACCATGCTCTAATCGTCA 39982
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AB109206 140715 bp DNA linear PLN 18-JUL-2003 Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 9, ARC clone: P0478E02.
AB109206 AB109202 AB109203 AB109205
AB109206.2 GI:32451478
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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2 (bases 1 to 140715)
2 (bases 1 to Mattos, L.T., Carvalho, F.F., Shimano, A., Zimmer, P.D. Malone, G. and Dellagostin, O.
                                                                                                                                                                                                                                                                                        GACCTGGCAGTGCTATAGAGCCGGCAGCCGGCTCTTCTATTAGCTTTGCTCTTATGGCTA
                                                                                               586 ACTATAGCTAATCTACA-GCCAGTTTATATATAAACAGGCTATAT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39983 GATCAATCTCTGATGTCG 40000
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AB109206
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TITLE

VERSION

COMMENT

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26615

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Direct Submission Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tesaski@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)

NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* This sequence will be replaced

* This sequence will be replaced

* This sequence will be replaced

* The accession number will be preserved.

* The accession number will be preserved.
                                                                                                                            26555
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                                                                                                                                                                                                                                                                                                                                                                                                                                  26676 AGGTGTACATGCGAATATTAAAT-----ATCTAAATCTTCAAAAGAGGTAAACA 26724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26725 AATAGCTAACCTAACAGCCAGTCTATTATATTATTGATGGCTATAGGTGACTACTA 26784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza sativa (japonica cultivar-group) chromosome 9 clone OSJNBA0087C18, *** SEQUENCING IN PROGRESS ***.
                                                                                406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      646
                                                                                                                                                                                                                                                                                 467 TAGCGATAGCACAAGCTCCCATGGAATCGAGCCAACATGCAACCGGCACAATGACTAAAG 526
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Oryza satīva (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae, Oryzeae; Oryza.
                                                                           347 ITTAGAGCAAGTATAATAAGTCCTAGTCAGCTGGCTATAAGATGTTCCACATCAGCAAAT
                                                                                                                                                                                                                               587 CTATAGCTAATCTACAGCCAGTTTATTATAAAACAGGCTATATAGCTGACCTGGCAGTG
                                                                                                                          26497 traagaggaggritaaracarccraarccecceccaacacacacaracacarcaacaa-
                                                                                                                                                                                                                                                                                                                                                                                 407 CCTTAAACTGGAGGAGAAAGAAGTAGGAGTGAGAAGGGCGTCGGCGCTTCGTCAATCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sasaki,T., Matsumoto,T. and Katayose,Y.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 9, BAC clone:OSJNBa0087C18
Published Only in Database (2002)
2 (bases 1 to 169030)
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                               Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       647 CTATAGAGCCGGCAGCCGGCTCTTCTATTAGCTTTGCTCTTA
     53.5%; Pred. No. 1.1e-07; ive 0; Mismatches 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sasaki,T., Matsumoto,T. and Katayose,Y. Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AP005970.1 GI:25815247
HTG; HTGS_PHASE2.
                               183; Conservative
       Local Similarity
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                                                                                                                                                                                                                                                 /trānslation="WVAKAACLPSAAAVALLLLAAAAAAGFAGATEYTVGDSEGWTIG
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AVGEPLPPPSPPPPPRAPFLAPPPPPVGSGAAAASSTWRRRRVALMVQVSCLALII
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ERREPREDABEQRPGRRYRLIAEIYAVTEEIE"
complement (44202.8"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="P0478E02.8"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="predicted by GeneMark.hmm etc."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40566 .40970
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/db_xref="GI:32526662"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="P0478E02.7"
                                                                                                                                                                                                                                                                                                                                                                              complement (34421.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon start=1
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Sasaki,T., Matsumoto,T. and Katayose,Y.

Direct Submission

Ly Submitted (26-DEC-2002) Takuji Sasaki, National Institute of Submitted (26-DEC-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan

(B-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)

On Jan 23, 2004 this sequence version replaced gi:27374998.

Genes were predicted from the integrated results of the following: Genes were predicted from the integrated results of the following: GENSCAN (http://CCR-081.mit.edu/GeneMark.hmm (http://www.softberry.com/), GeneMark.hmm (http://www.softberry.com/), GeneMark.hmm (http://www.softberry.com/), GeneMark.hmm (http://ppal.biology.gatech.edu/GeneMark.hmm), RiceHMM (http://ppal.biology.gatech.edu/GeneMark.hmm), RiceHMM (http://ppal.affrc.go.jp/RaceHMM/), SplicePredictor (http://ppoln.cse.psu.edu/html/docs/sim4.html), gap.cgi), sim4 (http://plobln.cse.psu.edu/html/docs/sim4.html), gap2 (http://www.tigr.org/software/glimmerm/), BlaSrN and BlaSrN. The genomic sequence was searched against NCBI NonRedundant Protein database at RGP or DDB4. Protein homologies of the coding regions were searched against NCBI NonRedundant Protein database with BlaSrP. ESTS represent the identified cDNA sequences using BlaSRN with the corresponding DDBJ accession no. and RGP clone ID. Full-length cDNAs represent the identified cDNA sequences using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77032 AGGIGIACAIGCGAATATIAAAI-----ATCTAAAICTICAAAAGGGGAAGAA 76984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76983 AATAGCTAACCTAACAGCCAGTCTATTATATTATTGATGGCTATAGGTGACATGGTACTA 76924
                                                                                                                                                                                                            77211 TTAAGAGCAGGTTTAATACATCCTAATCCGCCGGCGCTAGCACGCTACGCGTCAGCCAA- 77153
                                                                                                                                                                                                                                                                                                                                              77092 CCGGCTGAAGCGCAACACACAAAAAAGCTGCTTTCTTCCAACCAGATGCGAAGAATC 77033
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                                                                                                                                                                                                                                                                                  466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          587 CIATAGCTAATCTACAGCCAGTTTATTATAAACAGGCTATATAGCTGACCTGGCAGTG 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta, Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 9, BAC clone:B1274F11.
                                                                                                                                                                                                                                                                                                                                                                                                                        467 TAGCGATAGCACAAGCTCCCATGGAATCGAGCCAACATGCAACCCGCACAATGACTAAAG
                                                                                                                                                347 TTTAGAGCAAGTATAATAAGTCCTAGTCAGCTGGCTATAAGATGTTCCACATCAGCAAAT
                                                                                                                                                                                                                                                                                  407 CCTTAAACTGGAGGAGAAAGAAAGTAGGAGTGAGAAGGGCGTCGGCGCTTCGTCAATCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sasaki,T., Matsumoto,T. and Katayose,Y.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 9, BAC
Clone:B1274F11
Published Only in Database (2002)
2 (bases 1 to 171257)
                 Length 169030;
                                                                                 12;
5.7%; Score bz.c.,
53.5%; Pred. No. 1.1e-07;
*ive 0; Mismatches 147; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      647 CTATAGAGCCGGCAGCCGGCTCTTCTATTAGCTTTGCTCTTA 688
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                                                                                 Conservative
                                                 Similarity
                                                                                 Matches 183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              527
              Query Match
                                                    Best Local
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AP006149
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TITLE
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JOURNAL
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KEYWORDS
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..13633))
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5250, .5496,5578, .5654,6060, .6134,6207, .6308,6418, .6536,
6950, .7073,7170, .7220,7336, .7434,7928, .8088,9479, .9690,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MYQQLEYLNNSLSTNPTSNVHRQAALQLEIEVDRWYSAFCSLVK
SQRDYYSLITGWLRLSLFGGYHDPYNHAQNSDIYSLCEBWQLAIDRIPEDRYASEGIK
TLLTVIHAVVVQQAEEQKQKKRSESAFKELEKKAEELRSKYESLSSKYGPYSGAEGYGDMSR
KSPVSDKRAKVBALRGRADEBKSKYFKSIGYTRAMTLANLQTGFPNVFQAMTGFASVC
BLASTN with the corresponding DDBU accession no.

A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative' and '-like protein'. A gene without significant homology to any protein but with full-length cDNA or EST homology (covering almost the entire length of partial by two or more gene prediction programs is classified as an 'unknown' protein. A gene predicted by two or more gene prediction programs is classified as a 'hypothetical' protein according to IRGSP standard' A gene prediction program is also classified as a probable 'hypothetical' protein and is included as a miscellaneous feature of the sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="mgnggssgtlshsstveklyawekklflevkcsvasvsMicaml
LEFIEVKGSFQLYYYHGRDFLVLSMTAQLAQSYEGLKQEHDKKIGLLRKQEVKGVDYL
KMEKNKMEIESLDSKMLVATQSIETTTSEIMRLRESELFPQLLELVAGLVQ"
                                                                                                                                                                                                                                                                                                                                                                                                       The orientation of the sequence is from -21M13 to M13rev of the BAC clone. This sequence of B1274F11 has an overlap with P0229B10(DDBJ: AP006174) clone at 5' end and with P0478E02(DDBJ: AB109206) clone at 3' end. Detailed information on overlap and assembly quality together with annotation of this entry is available at http://rgp.dna.affrc.go.jp/GenomeSeq.html.
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5250. .5496,5578. .5654,6060. .6134,6207. .6308,6418. .
6950. .7073,7170. .7220,7336. .7434,7928. .8088,13290.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /Joce="Supported by full-length cDNA(s): AK068006"
complement(join(4062. 4453,4559. 4690,4807. 5160,
5250. 5506,5578. 5564,6600. 6134,6207. 6308,6418.
6950. 7073,7170. 7220,7336. 7434,7928. 8088,9479.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .171257
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/mol type="genomic DNA"
/cultivar="Nipponbare"
/db xref="taxon:39947"
/chromosome="9"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="B1274F11.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="B1274F11.2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       join(<622. .714,1056. .1147,1382. .>1658)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               product="hypothetical protein"
protein_id="BAD46562.1"
db_xref="G1:52076049"
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/product="hypothetical_protein"
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<2855. .>3583
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97514 AATAGCTAACCTAACAGCCAGTCTATTATTATTGATGGCTATAGGTGACATGGTA 97573
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                                                                                                                            /trānslation="MAAAASSSLAAAASSSRAAAVSARRAPSASPAAAASLPSPSRA
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LMKVPDKAVESRLDRRCTFVALGGGVIGDMCGFAAAAFLRGVNFIQIPTLMAQVDSS
                                                                                                                                                                                                                                                                   VGGKTGINHPLGKNI.IGAFYOPOCVLIDTETINTLPDRELASGIAEVVKYGLIRDAPF
FEWOEKNMPALLAREPSALAYAIKRSCENKAEVVAQDEKESGLRATLNIGHTFGHAIB
TGTGYGAWLHGEAVAAGTVWAADMSHRLGWIDESIKKRAIDILEKAKLPITPPEAMTV
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1 (bases 1 to 152423)
Wing, R.A., Frisch, D., Presting, G., Wood, T., Yu, Y., Soderlund, C., Kim, H.-R., Rambo, T., Henry, D. and Simmons, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wing, R.A., Frisch, D., Presting, G., Wood, T., Yu, Y., Soderlund, C., Kim, H.-R., Rambo, T., Henry, D. and Simmons, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                347 TTTAGAGCAAGTATAATAAGTCCTAGTCAGCTGGCTATAAGATGTTCCACATCAGCAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97345 ATTTGACGTGGAGGAGTGAGAAGGGAAGAAAAAGGATAGAGCGGGCGTTCCATCTATCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      467 TAGCGATAGCACAAGCTCCCATGGAATCGAGCCAACATGCAACCCGCACAATGACTAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97465 AGGTGTACATGCGAATATTAAAT-----ATCTAAATCTTCAAAAGAGGTAAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        587 CTATAGCTAATCTACAGCCAGTTTATTATATAAAACAGGCTATATAGCTGACCTGGCAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  407 CCTTAAACTGGAGGAGAAAGAAGTAGGAGTGAGAAGGGCGTCGGCGCTTCGTCAATCGC
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Submitted (11-APR-2001) Clemson University Genomics Institute,
Clemson University, 100 Jordan Hall, Clemson, SC 29634, USA
4 (bases 1 to 152423)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (14-SEP-2000) Clemson University Genomics Institute,
                                                                                                                                                                                                                                                                                                                                                                             EKFKSIMAVDKKVADGLLRLILLKGPLGSCVFTGDYDRNALDETLRAFCDC"
20888. .26689
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2 (bases 1 to 152423)
Wing,R.A., Frisch,D., Presting,G., Wood,T., Yu,Y., Rambo,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clemson University, 100 Jordan Hall, Clemson, SC 29634, USA ( bases 1 to 152423)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.7%; Score 62.8; DB 8; Length 171257;
llarity 53.5%; Pred. No. 1.1e-07;
Conservative 0; Mismatches 147; Indels 12;
                                product="putative dehydroquinate synthase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97574 GTATAGAGCCGGCAGGTGGCTATATTATTATCCTTGCTCTAA 97615
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                                                                 /protein_id="BAD46567.1"
/db_xref="G1:52076054"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="B1274F11.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC079853.2 GI:13384340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rice Genomic Sequence
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Oryza sativa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct
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es 183;
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Matches
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REFERENCE
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YGLKATVQYVQCPASPRTIKPLOPFFECFAKILVSLAMEANNYLYVVAKA
IPGLYRFVQFTIKKQVASWTLMPKTLEVPINDPSKASKKPWOTILLVKYLRAQNIRKKD
LLGKSDPYVALKASDKLPSKKTTVKRSLLNBEWNEDPRFFVVTDFFQLLIVFDWE
QVGKHEKMGNRNILLLKELPADETVWTVINLLKTMPENNESREGGLTEVTYRFK
EDDMEKEGIDNADVVEKAPDGTPAGGGLLYVVVHEAQDLEGKHTNPYAKIIFKGEEK
KTKVIKKNRDPRWENBEFEVCEBPPVNDKLHFRULSKASKKGLHGKETLGYIDISLA
DVISNKRINEKYHLIDSKWOGIQIDEWQWRTS"
join(12777. .12934,13027. .13124,13212. .13816)
/gene="Bl274Fil.4"
join(12777. .12934,13027. .13124,13212. .13816)
/gene="Bl274Fil.4"
/note="gene" plantylityling on the are not identified"
join(12777. .12934,13027. .13124,13212. .13816)
/gene="bl274Fil.4"
/note="gene" plantylityling on the are not identified"
/note="gene" plantyling on the are not identified"
complement (join (4325. 4453,4559. 4690,4807. 5160,
5220. 5496,5578. 5654,6060. 6134,6207. 6308,6418. 6536,
6950. 7073,7170. 7220,7336. 7434,7928. 8038))
/gene="B1274F11.3"
                                                                                                                                                                                                                                                                                                                                                                          /translation="MGVISTVLGFSGFGFGFSAGIVIGYYFFIYFQFTDVKDVKVRPL
VEYDSISLDGILPEIPLWVKNPDYDRIDWLNRFLEMMWPYLNKAICRTALDIAKPIIE
ENRKTYKLESIEFESLTLGSLPPFFQGMKVYVTEEQELIMEPSLKWAANPNVTVVVKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tränslation="maatgdaaavgeelraggrggtargltrropptrropgeelotg
Cgegvargrvogrcrrrggatvsarnkhmolosdgrslatdvreevkcsylrcsraas
Rtekaatgvpwgasrrkdlagsmpesrraaradaaqtaeraraaaaaavaasrstaac
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DHYVLRKVRDEEGREERKREDADVATLICGAHVDPTLSQLPHRIKPESKPLRASVMVD
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hote="supported by full-length cDNA(s): AK071977"
complement(join(1657. .17058,17236. .17379,17480. .17542,
18082. .18205,18868. .19094,19177. .19344,19437. .19587,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (join(16657. .17058,17236. .17379,17480. .17542,
18082. .18205,18868. .19094,19177. .19344,19437. .19587,
                                                                                                                                                                /note="contains EST(s): AU101494(E60352),AU030858(E60352)
contains full-length cDNA(s): AK068006,AK065681,AK068206"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="contains EST(s): AU056551(S20675),AU162699(S20675)
contains full-length cDNA(s): AK098959,AK071977"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <15612. .>16154
/gene="B1274F11.5"
/note="start and end point are not identified"
15612. .16154
/gene="B1274F11.5"
/note="contains EST(s): D23552(C2994),C71832(E0426)"
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/protein_id="BAD46564.1"
/db_xref="G1:52076051"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="unknown protein"
/protein_id="BAD46565.1"
/db_xref="G1:52076052"
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/gene="B1274F11.6"
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/db_xref="G1:52076053"
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18082. .182
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gene

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mRNA

mRNA

CDS

97404

526

97344

gene mRNA

CDS

466

97513

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32992. .36053
/gene="oSJNBb0004M10.5"
join(32992. .33231,33969. .34140,34322. .34475,34553. .34616,
34799. .34406,35083. .35208,35303. .35535,35831. .36053)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="butative calmodulin-like protein"
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GGISYHGSIPPRNSKYDPWGGPPLCSSCQLKKEAMEGKQHLTSMNFKLHDCAVCQLVMKFG
complement (37031...37604)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEGFVKYLVDSKLVFDTVERIVAESTDVAYVYFRKSGLERSARITKDLEWFGGGGIAV
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   'note="Similar to Micropon4 repeat sequence"
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/note="Similar to Class_4674 repeat"
22193. .22441
                                                                                                                                                                                                                                                                                                                                                                                                                        oxygenase 2"
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complement (8290. .11889)
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EQLCKKSALIJESVHFVHYPQPITVSRSECKCTPVRFFAIISSQSGSGWFFTLLNSH
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ARPTAPGHSPGAGHAFTNKNGVGRRLLVVTISTLI"
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                                                                                                      commuter, iterimi-zovi, temmson university denomics institute, clemson University, 100 Jordan Hall, Clemson, SC 29634, USA On Mar 20, 2001 this sequence version replaced gi:1012028.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality as compressions and repeats: all regions were covered by at least one plasmid subclone or more than one M13 subclone: and the assembly was confirmed by restriction digest. Within the assembly from 57011-57037 there are unresolved GC compressions.
Wing,R.A., Frisch,D., Presting,G., Wood,T.C., Yu,Y., Soderlund,C., Kim,H., Rambo,T., Henry,D., Simmons,J., Thurmond,S.K. and Mao,L. Direct Submission
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                                                                                             Submitted (12-MAY-2001) Clemson University Genomics Institute,
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/note="Similar to Explorer_Os1 MITE-like element"
18557. 18647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    342. .499
'note="Similar to pSINElr6 gene, repeat sequence"
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Oryza sativa chromosome 3 BAC OSJNBa0087G11 genomic sequence,
complete sequence.
                                              EELKHKLERAÄIDVDQAKQDSELAQLRÄQEMĒGGIDDEASVIAQTQLAVAKERHQKAV
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I EMVY I KEAETREKMAEL PKMLQQAAQEAEDAKVAPHSAQEELRKAKEEAEQTKAAAA
TAEIRLRAVLKEI EASKASEKLALVAAQALQESEETSSVEDSPRTITLPISEYHSLSK
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                                                                                                                                                                                                                        RVYEAEELANERVAAALAQIELAKESETRTÜERLQQETKEMHKKKDALQIALQRADRA
KEGKLGAEQELRKWRAELEQRRKAAKHVANPWTAPPIRSPEQKGSYKEDDAVLTEPNS
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Oryza sativa (japonica cultivar-group)
Bukaryoza, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 169728)
Buell, C.R., Yuan, Q., Ouyang, S., Liu, J., Gansberger, K., Jones, K.M., Overton II, L., Tsitrin, T., Kim, M.M., Bera, J.J., Jin, S.S., Fadrosh, D.W., Tallon, L.J., Koo, H., Zismann, V., Hsiao, J., Blunt, S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            147602 AAATCTGAC-GTGGAGGAGTGAGAAGGAAAAAAGGATGGAGCGGGCGTTCCATCTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLLLGAAAMDSSRRQADGADQVGGGVKEAGGIGGFVGLVALGDGSLSRN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 152423;
                                                                                                                                                                                                                                                                                             43860. .44040
/note="Similar to Tourist03 type MITE element"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                147374 CTAGTATAGAGCCGGCAGCTGGCTATATTATTATCCTTGCTCTGA 147330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches 149; Indels
                                                                                                                                                                                                                                                                           PMSNSSTDDFVVDQKLRKKKTFFPQMSSILSRKAQT"
                                                                                                                                                                                                                                                                                                                                                                                            /note="Hypothetical protein"
join(50104. .50332,50651. .50877)
/gene="OSJNBb0004M10.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 62.6; DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="Hypothetical protein"
/protein id="AAK52549.1"
/db xref="GI:14029008"
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                                                                                                                                                                                                                                                                                                                                           50104. .50877
/gene="OSJNBb0004M10.8"
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prediction programs including Egenesh (http://www.softberry.com/), genesan and Genesan+ (Chris Burge, http://www.softberry.com/), http://CCR-081.mit.edu/GENGCAN.html), GeneMarkHDM (Mark Borodovsky, http://GCR-081.mit.edu/GENGCAN.html), GeneMarkHDM (Mark Borodovsky, http://Genemark.biology.gatech.edu/GeneMark/), and GeneSplicer (Mihaela Pertea and Steven Salzberg, contact mpertea@itjer.org/, searches of the complete sequence against a peptide database and the plant EST database at TIGR (http://www.tigr.org/tdb/tgi.shtml). Annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE)). Simple repeats are identified by repeatmasker (Arian Smit, http://genome.wustl.edu/eddy/tRNAscan-SE)).
                                                                                                                                                                                                                                        Submitted (06-JUN-2001) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA (bases 1 to 169728)
                                                                                                                                                                                                                                                                                                                                                                              Medical Center Dr. Rockville, MD 20850, USA thases I to 169728)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BAC clone OSJNBa0087G11 is from Oryza sativa chromosome 3 The orientation of the sequence is from SP6 to T7 end of the BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genomic Research, 9712
Vanaken,S.S., Riedmuller,S.B., Utterback,T.T., Feldblyum,T.V., Yang,O.Q., Haas,B.J., Suh,B.B., Peterson,J.J., Quackenbush,J.,White,O., Salzberg,S.L. and Fraser,C.W.
Oryza sativa chromosome 3 BAC OSJNBa0087G11 genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (17-APR-2003) The Institute for Genomic Research, S
Medical Center Dr, Rockville, MD 20850, USA, rbuell@tigr.org
6 (bases 1 to 169728)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (23-APR-2003) The Institute for Genomic Research, Swedical Center Dr. Rockville, MD 20850, USA, rbuell@tigr.org On Apr 2, 2003 this sequence version replaced gi:20503084. Address all correspondence to:rice@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This BAC overlaps with rice BAC OSJNBb0004M10 (AC079853) and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Medical Center Dr. Rockville, MD 20850, USA 5 (bases 1 to 169728)
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/cultivar="Nipponbare"
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1300. .1343
/rpt_family="AT_rich"
complement(2402. .2977)
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/clone="OSJNBa0087G11"
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Location/Qualifiers
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Submitted (02-APR-2003)
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ERAAANKQWMPLLSPSLSEASLFSTKSAI TI NSVSTTAGSYSTGHYQHVARASSISPP
KSSQDKVCHDMLDTHVPEKSMSAVSNKDETSSVHFGYYTNRSDDEEEECSAYCSDRQV
                                                                                                                                                                                                                                                                                                                                                                /trānslation="MAAATNELQFVWVQLQAGSTVAXIGPWGGDYGGRDHDVTVAPRR
LRSVSLRHGKIIDSIAFTYDGGDGDGELHSVGPWGGDGAELPEAVARKLAAGERPPGA
TVAEFTFDAGERVTEVHGTVGPFGDRDSLVTSLKLVTDRRTIGPFGYGAGTPFSVPVR
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RRIVGGGAEEIGEAALMTAVTICEGRLLVEGRRGGEARGGGVVRGRWRIVGGSDDGAA
RGERGSGEPAMIAPCGFRGWERCAVGGAEQSLLLAPLSLPRGGWVRASGQRAPRAQGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translation="MACYLIGOTNKKIRKQKVLSGGRRGASLGALRVELVVLGGVGGD"
/note="similar to 15 kda organ specific salt induced procein GB:AAB23484 GI:256638 (Oryza sativa)" complement(<2402. .>2977)
/gene="GGJNBa0087G11.1"
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'protein_id="AAP12926.1"
'db_xref="GI:30017504"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="predicted by genemarkHMM"
join(<12537. 12600,13984. 14478,15561. .>15658)
/gene="05NDB00087G11.2"
join(12537. 12600,13984. .14478,15561. .15658)
/gene="05JNBa0087G11.2"
                                                                                                                                                                                                                                                      product="putative salt-induced protein"
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/db xref="GI:30017502"
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17665. 17688
17667. 19420
/rpc_family="AT_rich"
18398. 18420
/rpc_family="GC_rich"
1947. 19069
19444. 30211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene="OSJNBa0087G11.2"
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4017 ... 4040

/rpt_family="AT_rich"

4278 ... 4457

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6151 ... 6485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6151. .6172
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.2537. .15650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /rpt_family="GC_rich"
1840. .2922
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RYNPDSNGSNKVILDONILEAMPTSPIFVGRKAKRILERAVNDTAFTASIGWOYSIL
LVGVDEKKHELVWGIIDFMRQYTWDKHLETWVKTSGILGGPKNVAPTVISPKQYKMRF
RKAMSTYFLVVPDQWSPPAVVPSKQGAENNQDND"
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ISLHEGDETGWLEIVTSVSWEAANFIRPDTSQGGGMDPGGYVKFTYYLKPASNCFFST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           164615 AAATCTGAC-CTGGAGGAGTGAGAAAGGGAAGAAAAAGGATGGAGCGGCGTTCCATCTAT
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Oryza sativa (japonica cultivar-group) chromosome 5 clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 169728;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          family="T-rich"
4. .35762
family="AT_rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /rpt_family="AT_rich"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="hypothetical protein"
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16294. 16411,16668. 17455))
/gene="OSNNBb0111K12.2"
/codon_start=1
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KUGTVGAHLASGSWTLSREGCINKLLASRFRGDRLYLCDWPGCVHAEBRRKYWVRRGV
FHDPRSQVRRALRDTRRPTVAVDCAFCGCTEAWDLYAAFCLRSFYGYHDDGEBVVRA
YVCBNGHVAGAWTERPLYS"
                                                   /gene="OSJNBb0111K12.1"
/godon efert.
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join(24463. .24659,25048. .25309)
gene="OSJNBb0111K12.3"
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/db_xref="GI:46063430"
                                     /note="hypothetical protein"
complement(join(12540. 1256
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/gene="OSJNBb0111K12.2"
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/gene="OSJNBb0111K12.5"
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Direct Submission

Submitted (02-APR-2004) Institute of Botany, Academia Sinica, 128, Section 2, Academia Road, Mankang, Tabjea 11529, Taiwan

On Jul 2, 2003 this sequence version replaced gi:3218941.

The orientation of the sequence is from Sp6 to T7 of the BAC clone. Genes were predicated from the integrated results of the BAC clone. BLASTA2.0, GENSCAN (Chris Burge, http://genes.mit.edu/GENSCAN.html), Fgenesh (http://www.rigr.org/softlab/glimmer/glimmer.html), TWINSCAN (http://www.tigr.org/softlab/glimmer/glimmer.html), TWINSCAN (http://www.tigr.org/softlab/glimmer/glimmer.html), TWINSCAN (http://www.tigr.org/softlab/glimmer/glimmer.html), TWINSCAN (http://www.tigr.org/softlab/glimmer/glimmer.html), TWINSCAN (http://www.tigr.org/tdh/Genesplicer/index.shtml), TWINSCAN (http://www.tigr.org/softlab/glimmer/glimer.html), TWINSCAN (http://www.tigr.org/softlab/glimmer/glimer.html), TWINSCAN (http://chaol.dna.affrc.og.jp/cDNA/). Annotated genes are named to laill-length cDNA database (KoME, http://chaol.dna.affrc.go.jp/cDNA/). Annotated genes with similarity are named as unknown proteins. Genes without proteins are named after the database hits. Genes without are proteins are named after than two gene prediction programs over most of their length are annotated as hypothetical proteins. This clone overlaps with P0683B02 (accession # AC135927) and OsJNBa0090002 (accession # AC137618).
                                                                                                                                                    Oryza sativa (japonica cultivar-group)

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Enrhartoideae; Oryzeae; Oryza.

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E (basea: Oryzeae; Oryza.

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Chow, T.-Y. and Hsing, Y.-I.C.
Direct Submission
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Chow,T.-Y. and Hsing,Y.-I.C.
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Chow,T.-Y. and Hsing,Y.-I.C.
Direct Submission
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/mol type="genomic DNA"
/cultivar="Nipponbare"
/cultivar=axon:39947"
/chromosome="S"
/clone="0SJNBb0111K12"
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OSJNBb0111K12, complete sequence.
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AC121366.4 GI:32401478
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39669. .40019)
/gene="05JNBb0111K12.6"
/note="similar to rice EST AK120909"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(join(43031. .43218,43419. .44252,44326. .46939))
/gene="OSJNBb0111K12.7"
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VGPGGMGKSTLAQYYYNDKTIQEHFDVTMWVCISRKLDVHHHTREIIESATKEKCQRV
GNMDVLQYKLKEILQKKEKVLLVLDDIWFDKSQDVEEWDLLLAPILSSQNGATKVLVT
SRSKTLPPALFSEDVIDLENMKDTEGALFKHHAFGATIRDLQMCGWFEEHAVKITE
RLGRSPLAAKVVGSHLKRVMNIDDWKGALFKHHAFGATIRDLQMCGWFEEHAVKITE
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/translation="MALPLLSSPLTSSIKLWTRPSRARREPLPLAAGALEPANTTPTR
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TVSGDPVGTPGSFGNMADYNVHLHQPDBGDDHGDSTECSSSFGPSCSASSDDDDDTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DTVDTSLYLKRHPALSYYENKNSGVQTDGPLVNGGFDSSVVEDIESTDDALVENDRVF
EQYSLREIILITVDDVQSRILSLGCGRLSNARSKYKKLSQCLDRKQVKVPQKIQNQMTCC
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LNG1T1EMFCGKDNFLTNAHVGELYKESADDVLJDNQAAKEGYQLFEKVKPEEHSELV
MPPSKVQKASADIVDYEQVQETAPVAKQ1ISGDKRGQKPNKKHGLPVLAKKIKTEKDP
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KOHINATLICIDPLVDVGSNIFBQVVLNLKKLQVLYLSFYNTKLPSEIGQLKHLRYL
NIKKTLISELPRSLCDLYHLELLYLRPKSRLPDKLCNLCKLRHLQMYSDGLELSRIPD
IGRLTLLQRIDSFHLUKQKGHELRQLNNNNEIGSYLSLANLENVIGKDBALESKLYQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NLLSQVAKYDRELAIINHEKDLQLEMVKADGPKSEPGKLYPQSHERIIMKRRKRKRDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
/product="putative disease resistance protein, contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="OSJNBbb111K12.7"
/note="putative disease resistance protein, contains
NBS-LRR domain"
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                                                                                                                                                                                                                                                                                                                                                                                /product="unknown protein"
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/db_xref="G1:46063431"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="AAS79735.1"
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                                                                                                                                        gene="OSJNBb0111K12.6"
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PLN 03-JUN-2004

linear

DNA

135231 bp

AC137618

RESULT 15 AC137618 LOCUS

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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enrhartoideae; Oryzeae; Oryza.

Enrhartoideae; Oryza.

Enrhartoideae; Oryzeae; Oryza.

Chases 1 to 135211

Chow, T.-Y., Hsing, Y.-I.C., Chen, R.-K., Chen, H.-H., Liu, S.-M., Chen, Y.-T., Chang, S.-J., Chen, R.-C., Chen, S.-K., Chen, T.-R., Hsing, Y.-I.C., Chen, S.-Y., Hsiao, S.-H., Huang, J.-N., Hsu, C.-H., Huang, J.-J., Kau, P.-I., Lie, M.-E., Lin, S.-W., Wu, H.-P. and Shaw, J.-F.

Oryza sativa BAC OsJNBa0090H02 genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            346 GITTAGAGCAAGTAIAATAAGTCCTAGTCAGCTGGCTATAAGATGTTCCACATCAGCAAA 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            406 TCCTTAAACTGGAGGAGAAAGAAAGTAGGAGTGAAAGGGCGTCGGCGCTTCGTCAATCG 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
2. (Dases 1 to 135231)
Chow T.-Y. and Hsing, Y.-I.C.
Direct Submission
Direct Submission
Submitted (27-NOV-2002) Institute of Botany, Academia Sinica, 128, Section 2, Academia Road, Nankang, Taipei 11529, Taiwan
(bases 1 to 135231)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission Submission Submitted (03-JUN-2004) Institute of Botany, Academia Sinica, 128, Section 2, Academia Road, Nankang, Taipei 11529, Taiwan On Jun 3, 2004 this sequence version replaced gi:25696256.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Gaps
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Corganism="Oryza sativa (japonica cultivar-group)"
/mol type="genomic DNA"
/cultivar="Nipponbare"
/db xref="teaxon:39947"
/chromosome="5"
/chromosome="5"
/chore="65"
/chore="65"
Oryza sativa (japonica cultivar-group) chromosome 5 clone OSJNBa0090H02, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 5.3%; Score 59.4; DB 8; Length 135231; Best Local Similarity 73.6%; Pred. No. 1.4e-06; Matches 89; Conservative 0; Mismatches 31; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: August 30, 2005, 15:16:34 Job time : 5152 secs
                                                                         AC137618.2 GI:48055771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chow, T. -Y.
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     DEFINITION
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JOURNAL
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

August 30, 2005, 05:58:55; Search time 700 Seconds (without alignments) 9395.475 Million cell updates/sec Run on:

US-09-979-549-2

1 gaagtcagaaggccgttcag........ Title: Perfect score:

Sequence:

Scoring table:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0

4390206 segs, 2959870667 residues Searched:

8780412

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N_Geneseq_16Dec04:* Database

genesequ1980s:* genesequ1990s:* genesequ2001as:* genesequ2001as:* genesequ2002as:* genesequ2003as:* genesequ2003as:* genesequ2003as:* geneseqn2003ds:* geneseqn2004as:* geneseqn2004bs:* geneseqn2003cs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

•	`	oko (SUMMARIES	
Result No.	Score	Query	Query Match Length DB	DB	ID	Description
-	1111	100.0	2687	S	AAC84132	
0	57.8	5.5	2000	ω,	ADA72361	Ada72361 Rice gene
w 4	47.8	4. 4. 	9539	φ¢	AAS20135 AAS20019	Aas200135 Genomic D Aas20019 Genomic D
	45.8	4.1	1976	12	ADJ44967	Adj44967 Plant cDN
9	41	3.7	1999	10	ADC08428	Adc08428 Rice DNA
7	39.8	3.6	2000	8	ADA71571	Ada71571 Rice gene
σ,	39.4	3.5	69300	9	AAD38804	Aad38804 BAC clone
9	38	3.4	24333	12	ADJ12497	Adj12497 DNA fragm
70	38	3.4	24333	12	ADJ12606	Adj12606 DNA fragm
11	37.2	3.3	88191	۵	ABX14763	Abx14763 Genomic D
12	36.6	3.3	2000	۵	ADA71938	Ada71938 Rice gene
13	36.2	3.3	1898	11	ACN91201	Acn91201 Breast ca
14	36.2	3.3	2000	10	ADC08414	Adc08414 Rice DNA
15	36.2	3.3	5955	12	ADH22268	Adh22268 Rice PONG
16	35.8	3.2	460	m	AAC28189	Aac28189 Human sec
17	35.2	3.2	2000	œ	ADA71938	
18	35	3.2	704	9	ABQ32010	Abq32010 Oligonucl
19	35	3.2	704	9	ABQ32011	Abq32011 Oligonucl
20	34.8	3.1	7525	4	AAS01192	Aas01192 Fertilisa

Adc29908 Fertiliza Adm39442 Maize ZmF Abc35188 Olidonucl	Abq35189 Oligonucl	Aa846329 lumour Bu Abk31246 Signal tr	Abl70201 Chemicall	Aas61159 Human gen	Acn44586 Human gen	Adk52808 Plant DNA	Adr64189 Cotton cD	Abi99351 Mouse isc	Ade84216 Human lym	Ads89620 Oligonucl	Abd33282 Murine ca	Adr67037 Mouse can	Abv59185 Human pro	Adre0416 Cotton cD	Abq92787 Triticum	Aba90875 Bacillus	Aak69744 Human imm	Aas34694 Human DNA	Abv15204 Human pro	_	Abq33210 Oligonucl
ADC29908 ADM39442 ABO35188	ABQ35189	AAS46329 ABK31246	ABL70201	AAS61159 .	ACN44586	ADK52808	ADR64189	AB199351	ADE84216	ADS89620	ABD33282	ADR67037	ABV59185	ADR60416	ABQ92787	ABA90875	AAK69744	AAS34694	ABV15204	ABQ33211	ABQ33210
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ALIGNMENTS

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Wheat; TaTrxh2; thioredoxin; promoter; gene expression; transgenic plant; monocotyledon; plant cell; seed; amylaceous albumen; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                        /function= "possible regulator of gene expression in
response to abscist; acid"
/note= "present in thioredoxin h gene promoter sequences
from tobacco and rice"
                                                                                                                                                                                                                                                                    /*tag= c
/label= Gibberellic_acid_response_element
/function= "regulates gene expression in response to
gibberellic acid"
699. .708
                                                                                                                                                                                                                                        t
                                                                                                                                                                                                                  /*tag= b
//label= Glbberellic_acid_response_element
//label= Glbberellic_acid_response
glbberellic_acid"
561. .569
                                                                                                                                                                                   /*tag= a
/note= "promoter region is specifically claimed"
550. .558
                                                                                                                                                                                                                                                                                                                                                                     /*tag= e
/bound_moiety= "leucine zipper proteins"
/label= bzip_motif
867. .883
                                                                                                                                                                                                                                                                                                                                     /bound_moiety= "GCN4-like protein"
/label= GCNA-like_box
                                                                                                                                                       Location/Qualifiers
1...1111
                       AAC84132 standard; DNA; 2687 BP.
                                                               (first entry)
                                                                                     Wheat TaTrxh2 gene.
                                                                                                                                         Triticum aestivum.
                                                                                                                                                                                                                                                                                                                 protein_bind
                                                                                                                                                                                                                                                                                                                                                           protein_bind
                                                               09-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                    misc_signal
                                                                                                                                                                                                         misc_signal
                                                                                                                                                                                                                                                              misc_signal
                                          AAC84132;
                                                                                                                                                                           promoter
RESULT 1
AAC84132
ID AAC84
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9 9 120 120 180 180 240

240 300 300 360 360 420 420 480 480

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CATCTGAACCGTTCAACAGCCCCACGTAATTTCGCGCACCAGCAAGGGCATATCCGTCA 960
to control gene expression in transgenic plants (particularly monocotyledons) or plant cells, especially for seed-specific expression, particularly in the amylaceous albumen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAGCCAGTTTATTATAAACAGGCTATATAGCTGACCTGGCAGTGCTATAGAGCCGGCA
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                                                                                                                                                                                                               61 AGACGACGGGGGGCATGTGCCTGTTGGCGAGGCGTCTAGCTTTGGCAGCCGCCGC
                                                                                                                                                                                                                                  AGACGAGGCGGCATGTGCTTCCTTGGCGAGGCGTCTAGCTTTGGCAGCCGCCGC
                                                                                                                                                                                                                                                                         CGCTTTTCTCCTTGGGTGGGCGCGCGAGCTCCCCGAGTTTGAGCCGCAATTTTTTACAT
                                                                                                                                                                                                                                                                                            CGCTTTTCTCCTTGGGTGGGGGGGGGGGTCCCCGGAGTTTGAGCGGCAATTTTTTACAT
                                                                                                                                                                                                                                                                                                                                   TITATCGCGATGGCGTCAGGCGTTTATCTAGGCGTCTGGGAGGGTACATTTGAAGATGTG
                                                                                                                                                                                                                                                                                                                                                                                               CCACCAACTCCAAACCGACAACCCTGTATCTGAGCATGCCTCATGCCTCTCCTTCATGCC
                                                                                                                                                                                                                                                                                                                                                                                                                             ccaccaactccaaaccaacaacctcrareraagcareccrcareccrcrrcarecc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGCCAGTTTATTATATAAACAGGCTATATAGCTGACCTGGCAGTGCTATAGAGCCGGCA
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                                                                                                                         ;
                                                                                           Length 2687;
                                                             Sequence 2687 BP; 638 A; 626 C; 690 G; 733 T; 0 U; 0 Other;
                                                                                                                         Indels
                                                                                                                       .;
0
                                                                                           DB 5;
                                                                                         100.0%; Score 1111;
100.0%; Pred. No. 0;
ive 0; Mismatches
                                                                                         Query Match
Best Local Similarity 100.
Matches 1111, Conservative
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                      /*tag= g
dound_moiety= "basic helix-loop-helix transcription
factor"
                                                                                                                                                                      function= "involved in aleurone layer-specific gene
                                                                                                                                                                                                                                                                *tag= k
function= "involved in aleurone layer-specific gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New promoter from a wheat thioredoxin gene, useful for controlling transgene expression in plants, provides seed-specific expression.
                                                                                                                                                                                                                                                                                          xpression"
021. .1028
*tag= 1
bound molety= "Sp1 transcription factor"
label= GC_box
                                                                                                       bound moiety= "leucine zipper proteins"
label= bzip_motif
001. .1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (S'site:YES, 3'site:NO)
                                                                'label = bHLH_recognition_motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                           product= "thioredoxin h2"
note= "CDS contains introns"
232. 2202
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*tag= j
note= "TATA-like box"
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gene= "TaTrxh2"
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1047. .1231
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2429. .2687
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/number= 3
2558. .2687
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/*tag= p
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2584. .2589
                                                                                                                                                                                    expression"
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/*tag= q
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    906.
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P-PSDB; AAB37102.
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   protein_bind
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840 900

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encoding fructosyl transferase homologue, Lp6SFT1 version 2.
                                                                                                                                                                                                                    Fructosyl transferase homologue; Lp6SFT1; perennial ryegrass; fescue; fructan biosynthesis; forage; turf grass improvement; deforment; dery matter digestiblity; herbage quality; palatability; cold tolerance drought tolerance; tiller survival; plant persistence; abiotic stress; low calorie sweetener; ds.
                                                                                                                                                                                                                                                                                                                                                                         "Lolium perenne fructosyl transferase"
                                      449 CGGCGCTTCGTCAATCGCTAGCGATAGCACAAGCTCCCATG 489
                                                        285 GGACGCTTATTTAAGCGCTAGCGCTAACAATAAACAATG 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Terdich K;
                                                                                                                                                                                                                                                                                                                                                                                              note= "No stop codon given"
trans1 except= (pos:7176. .7186,
702. .5112
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UNIV ADELAIDE.
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STATE SOUTH AUSTRALIA SOUTH AUSTRALIAN
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                                                                                                                                                                                                                                                                                                                            location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                               "Lp6SFT1"
                                                                                                                          AAS20135 standard; cDNA; 9538
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/number= 3
7613. .9055
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6113. .6327
/*tag= c
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/number= 3
9056. 9457
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/number= 2
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                             TAGCGAGCGCATAAATITCTGATTCCTGCCTGCCTGCCGGACAATTTATCTTTGGGAGGC 1020
                                                                             The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to illustrate the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             404 GCGGCTAGGAGCAGTGCTGGTAGAGAGTACAATAAG-CCTAGTCAGCTGGCGGCAAAA 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCGCCGAGTGCCTTCCCCGTTTAGAGCAAGTATAATAAGTCCTAGTCAGCTGGCTATAAGA
                                                             GGGCCGGGATTGGAGACAGAGCCCACAAGAGCAACAAGAGTGCGCGTGAGAAATCAACA
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Whitham S, Xie Z, Zhu T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57; Indels
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Pred. No. 1.4e-07;
0; Mismatches 57;
                                                                                                             AGCGGTGCTTGCCGAGAGAGAGAGAGAGAG 1111
                                                                                                                           AGCGGTGCTTGCCGAGAAGAGAGAGAGAGAGAGAG 1111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SYGN ) SYNGENTA PARTICIPATIONS AG.
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S, Tao Y,
                                                                                                                                                                                                  ADA72361 standard; DNA; 2000
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Katagiri F, Quan S,
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es 103; Conserv
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Matches
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350 AGAGCAAGTATAATAAGTCCTAGTCAGCTGGCTATAAGATGTTCCACATCAGCAAATCCT 409
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                                                                                                                    exon
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                                                                                                                                                                                                      Transmittor describes a mover purities of the polymuclectide and a vector encoding it are useful for andifferase homologue from a ryegrass (Lolium sp.) or fescue (Festuca sp.). The polymuclectide and a vector encoding it are useful for amodifying fructan biosynthesis in a plant.

Regulatory elements isolated from the gene are useful for expressing an exogenous gene in plant cells. The nucleic acid is useful as a molecular genetic marker for qualitative trait loci (QTL) tagging, QTL mapping, DNA fingerprinting and in marker assisted selection, in forage and turf grass improvement, e.g. tagging QTLs for dry matter digetibility, herbage culting and grazing, cold tolerance, drought tolerance, tiller survival and plant persistence. Modification of fructan biosynthesis leading to fructan accumulation fructans produced by the plants are also useful as low calorie sweeteners. This the genomic DNA sequence encoding the Lolium perenne fructans transferase homologue, Lofskri, isolated from perennial ryegrass using an Lp66FrI cDNA probe, described in the method of the invention. Note: This sequence differs from Lp65FII version I (AAS20019)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8049 CTAGTIGGAGGAGAGATAGGAGGAGAGA-ATGTGAGTATGCTCTTATGCAAGAGCTAG 8107
                                            Novel nucleic acid encoding fructosyl transferase homolog from ryegrass or fescue species useful for modifying fructan biosynthesis in plants and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fructosyl transferase homologue, Lp6SFT1; perennial ryegrass; fescue; fructan biosynthesis; forage; turf grass improvement; dary matter digestibility; herbage quality; palatability; cold tolerance; drought tolerance; tiller survival; plant persistence; abiotic stress; low calorie sweetener; ds.
                                                                                                                                                                                       invention describes a novel purified or isolated nucleic acid or its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomic DNA encoding fructosyl transferase homologue, Lp6SFT1 version 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          410 TAAACTGGAGGAGAAAGAAAGTAGGAGTGAAAAGGGCGTCGGCGTTCGTCAATCGCTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9538 BP; 2084 A; 2600 C; 2397 G; 2369 T; 0 U; 88 Other;
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5702. .9458
/*tag=
/product= "Lp6SFT1"
/note= "Lolium perenne fructosyl transferase"
/partial
/partial
/note= "No stop codon given"
5702. .6112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.3%; Score 47.8; DB 6; Length 9538; 52.9%; Pred. No. 0.00074; lve 0; Mismatches 52; Indels 1
                                                                                                                                          Disclosure; Page 57-65; 139pp; English.
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                                                                                              as a molecular genetic marker.
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Conservative
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shown in figure 10
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The invention describes a novel purified or isolated nucleic acid or its fragment encoding a fructosyl transferase homologue from a ryegrass (Icolium sp.) or fescure (Restuca sp.). The polynucleotide and a vector encoding it are useful for modifying fructan biosynthesis in a plant. Regulatory elements isolated from the gene are useful for expressing an exogenous gene in plant cells. The nucleic acid is useful as a molecular genetic marker for qualitative trait loci (QTL) tagging, QTL mapping, DNA fingerprinting and in marker assisted selection, in forage and turf grass imperprinting and in marker assisted selection, in forage and turf grass improvement, e.g. tagging QTLs for dry matter digestibility, herbage (unality, palatability, regrowth after cutting and grazing, cold tolerance, drought tolerance, tiller survival and plant persistence. Modification of fructan biosynthesis leading to fructan accumulation fructans produced by the plants are also useful as low calorie sweeteners. This the genomic DNA sequence encoding the Lolium perenne reconstructory transferase homologue, Ip6SFT1, isolated from perennial ryegrass using an Lp6SFT1 cDNA probe, described in the method of the invention. Note: This sequence differs from that of Lp6SFT1 version 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel nucleic acid encoding fructosyl transferase homolog from ryegrass or fescue species useful for modifying fructan biosynthesis in plants and as a molecular genetic marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9539 BP; 2085 A; 2602 C; 2397 G; 2369 T; 0 U; 86 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spangenberg GC, Lidgett AJ, Johnson XA, Terdich K;
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INT MAIZE & WHEAT IMPROVEMENT CENT.
STATE SOUTH AUSTRALIA SOUTH AUSTRALIAN
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/*tag= e
/number= 2
6774...7613
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7614. .9056
/*tag= 9
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9057. .9458
/*tag= h
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                                                     // (113. .6327
/*tag= c
/number= 1
6328. .6336
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/*tag= b
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P-PSDB; AAU74399.
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Best Local Similarity
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Gaps

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Indels

0; Mismatches

Conservative

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Glazebrook J,
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11D ADC0842
AC ADC0842
AC ADC0842
AX ADC0842
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                                                                                                       8108
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plant; gene; ss; transcription; plant genome augmentation; cereal; soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet; maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance; stress tolerance; salt tolerance; cold tolerance; drought tolerance; plant nutrition; apical dominance; dwarfism; early flowering; antiviral;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to plant nucleotide sequences that direct seed-, leaf- and/or stem-, panicle-, root- or pollen-specific or -preferential or constitutive transcription of an operatively linked nucleic acid segment. The invention also relates to a method for augmenting a plant genome and a method of identifying a gene, where its expression is attered in the seed, leaf, stem, panicle, pollen, root or is constitutive in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower, canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New rice promoter, useful for manipulating crop plants to alter or improve phenotypic characteristics, e.g. produce large quantities of oil or proteins, resistance to insecticides, virus or fungi, stress tolerance or high nutritional value.
CTAGTUGGAGGAGGAGGAGGAGAGA-ATGTGAGTATGCTCTTATGCAAGAGCTAG
                                                             TAAACTGGAGGAGAAAGAAAGTAGGAGTGAGAAGGGCGTCGGCGCTTCGTCAATCGCTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glazebrook J;
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tagiri F, Kreps J, Provart N, Ricke D, Zhu T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 26; SEQ ID NO 5967; 230pp; English.
                                                                                                                                                                                 crcraccaccrccraccca 8131
                                                                                                                                             CGATAGCACAAGCTCCCATGGAA 492
                                                                                                                                                                                                                                                                                        ADJ44967 standard; cDNA; 1976 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-SEP-2001; 2001US-0325277P.
26-SEP-2001; 2001US-0325448P.
04-APR-2002; 2002US-0370620P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BRIGGS S P.
COOPER B.
GLAZEBROOK J.
GOFF S A.
KATAGIRI F.
KRERS J.
PROVART N.
RICKE D.
                                                                                                                                                                                                                                                                                                                                                                      (first
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                                                                                                                                                                                                                                                                                                                                                                                                              Plant cDNA #5967
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antifungal.
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                       7990
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                                                                                                                                                                                                                                                                                                                              ADJ44967;
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(RICK/)
(ZHUT/)
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(BRIG/)
(COOP/)
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(GOFF/)
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(KREP/)
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sorghum, rice or wheat. The polynucleotides and the polypeptides they encode are useful for manipulating crop plants to alter or improve phenotypic characteristics, to produce large quantities of oil or proteins, to incur resistance to insecticides, viruses or fund; and to incur stress tolerance (e.g. salt, cold or drought) to ensure the plants have a high nutritional value with reduced apical dominance or dwarfism, early flowering or alterered metabolic pathways. This sequence represents a plant nucleic acid of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;
carbohydrate degradation; carbohydrate; plant grain; grain filling; corn;
tomato; banana; canola; cotton; paanut; sorghum; tobacco; sugarbeet;
wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New plant genes encoding polypeptides having an activity involved in or associated with the synthesis, metabolism or degradation of carbohydrates in the plant grain useful in generating plants having improved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  348 TTAGAGCAAGTATAATAAGTCCTAGTCAGCTGGCTATAAGATGTTCCACATCAGCAAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           408 CTTAAACTGGAGGAGAAAAAAAAGTAGGAGTGAGAAGGGCGTCGGCGCTTCGTCAATCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention, in the area of plant biotechnology, relates to novel
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Ricke D;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1976;
                                                                                                                                                                                                                                                                                                                                                                    Sequence 1976 BP; 489 A; 464 C; 447 G; 576 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                468 AGCGATAGCACAAGCTCCCATGGAATCGAGCCAACATGCAACCCG 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          577 edercejageereeraceeageejaaageeeeereeeagee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rice DNA sequence Seq ID733 related to grain filling.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 45.8; DB 12;
Pred. No. 0.0014;
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Provart N,
                                                                                                                                                                                                                                                                                                                                                                                                         4.1%; Sco...
58.8%; Pred. No. co...
7. Mismatches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kreps J,
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26-SEP-2001; 2001US-0325277P.
20-DEC-2001; 2001US-0342327P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADC08428 standard; DNA; 1999
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Katagiri F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 58.8
Matches 97; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene; ds; plant
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useful for conferring resistance to resistance or tolerance to a plant to

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polynucleotides comprising a nucleotide sequence encoding a protein which is involved in or associated with the synthesis, metabolism or degradation of carbohytates in the plant grain and the expression of which is up-regulated during grain filling. The plant is selected from corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco, sugarbeet, wheat, and rice. The invention may be useful for the improvement of protein, oil, starch, fibra and moisture content of the cereal grains. In addition, carbohydrate levels may be modified to a more desirable level using the present invention. The present sequence is a DNA sequence of a rice gene promoter. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fite, wipo.int/pub/publishedpct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                       687
                                                                                                                                                                                                                                                                                                                                                                                                     282 TATAGATGACATGGTAGTATTCAGCCAGCAGCCGGCTAAAGTATTAGCCTTGCTCTT 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant
                                                                                                                                                                                                                                                                                                                                                                     628 TATAGCTGACCTGGCAGTGCTATAGAGCCGGCAGCCGGCTCTTCTATTAGCTTTGCTCTT
                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plant; bacterial infection; fungal infection; viral infection; rice;
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                                                                                                                                                                                                                                                                                            3.7%; Score 41; DB 10; Length 1999; llarity 72.6%; Pred. No. 0.054; Conservative 0; Mismatches 20; Indels
                                                                                                                                                                                                                                                            Sequence 1999 BP; 624 A; 366 C; 428 G; 580 T; 0 U; 1 Other;
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Zhu
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Whitham S, Xie Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 27; SEQ ID NO 4894; 899pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGGAGGGGATGTG 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGGCTACATCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rice gene, SEQ ID 4894
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                                                                                                                                                                                                                                                                                                                 Local Similarity
les 53; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2003000898-A1.
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Katagiri F,
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                                                                                                                                                                                                                                                                                                                                                                                                                                             688
                                                                                                                                                                                                                                                                                                   Query Match
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Matches
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The invention relates to a polynucleotide isolated from chromosome 11 of Indica rice cultivar C039, flanked by marker R2316 and RG1094 comprising one or more genes that confer resistance to strains of Magnaporthe grisea having avirulence gene AVR1-C039. The pi-C039(t) polynucleotides are useful for conferring or improving resistance of plants to strains of the rice blast pathogen, Magnaporthe grisea and other pathogens. The Pi-C039(t) nucleic acids may be used as probes to detect the presence of and/or expression of Pi-C039(t) genes, and to products of Pi-C039(t) proteins. Purified gene products of Pi-C039(t) are useful in producing polyclonal or monoclonal antibodies useful as sensitive detection reagents for the presence and accumulation of Pi-C039(t) properties. The transgenic plants are useful for plant breeding or directly in agricultural or horticultural applications. The present sequence is BAC clone E2P5 from rice variety C039
                                                                                                                                  o;
                                                                                                                                                                    329 GCGGCGAGTGGCTTCCCGTTTAGAGCAAGTATAATAAGTCCTAGTCAGCTGGCTATAAGA 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New PiCO39(t) polynucleotides from chromosome 11 of Indica rice cultivar CO39 useful for conferring or improving resistance of plants to strains of Magnaporthe grisea or other plant pathogens with avirulence gene AVR1-CO39.
                                                                                                                                                                                       fungal or viral infection. The present sequence was used to
                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rice; chromosome 11; Indica rice cultivar; CO39; avirulence gene; AVR1-CO39; rice blast pathogen; transgenic plant; plant breeding; resistance; agricultural; horticultural; plant protectant; ds.
                                                                                                                                  ·,
                                                                                                 Length 2000;
                                                               Sequence 2000 BP; 585 A; 533 C; 403 G; 479 T; 0 U; 0 Other;
                                                                                                                                27; Indels
                                                                                              Score 39.8; DB 8;
Pred. No. 0.13;
0; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chauhan RS, Durfee TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 4; Page 110-142; 175pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SAC clone E2P5 from rice variety CO39.
                                                                                                                                                                                                                                         389 TGTTCCACATCAGCAAATCCTTA 411
                                                                                                                                                                                                                                                             31 TTTCCCACGTCATCAAAATCCTA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (WISC ) WISCONSIN ALUMNI RES FOUND. (USDA ) US DEPT OF AGRICULTURE.
                                                                                                                                                                                                                                                                                                                                                                 AAD38804 standard; DNA; 69300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-OCT-2000; 2000US-0242313P. 09-JUL-2001; 2001US-0303897P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-OCT-2001; 2001WO-US046331
                                                                                                                  67.5%;
                                                                                                   3.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                    23-SEP-2002 (first entry)
                                                                                     illustrate the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryza sativa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-MAY-2002.
                  bacterial,
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Rosen CA,
Young PE,
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                                                                                                                                                                                                                                                     human, secreted; cancer; haematopoietic disease; anaemia;
multiple myeloma; reproductive system disorder; prostatitis;
multiple myeloma; reproductive system disorder; prostatitis;
multiple myeloma; reproductive system disorder;
multiple myeloma; reproductive systemic lupus erythematosus;
gout; cardiovascular disease; arrhythmia; hypernatraemia; fetal disease;
merial alcohol syndrome; Down's syndrome; excretory disease;
murinary incontinence; renal disorder; neural; sensory disease;
multiple mer's disease; empirities; endering disease; endering disease; endering disease; endering disease; portal hypertension;
multiple bowel syndrome; epithelial disease; scleroderma;
pridermolysis bullosa; cytostatic; antianemic; antianthritic;
multiple bowel syndrocerive; antianemic; antianthritic;
multiple for antiarrhythmic; cardiant; noctropic; antilipemic;
menhororiolis; uniparhic; neuroprotective; antiparkinsonian; tranquilizer;
multidiabetic; anabolic; hypertensive; vulnerary; ds.
                                                                               35667 CAGCCGGCCTATTATATAAGTGAAGGCTTTAGGTGATGTGTCTCACTAGTATAACGCCCACT 35726
                                                            601 CAGCCAGTTTATTATATAAACAGGCTATATAGCTGACCTGGCAGTGCTATAGAGCCGGCA 660
                                                                                                                                                                                                                                       DNA fragment of a BAC clone that encodes a human secreted protein Seq351
 Sequence 69300 BP; 19720 A; 15094 C; 15006 G; 19380 T; 0 U; 100 Other;
                                        Gaps
                                        ö
                   Score 39.4; DB 6; Length 69300;
Pred. No. 1.5;
0; Mismatches 31; Indels 0;
                                                                                                             35727 GCTGGCGTTCTTATTATCCTTGCTCTTAT 35755
                                                                                                    661 GCCGCTCTTCTATTAGCTTTGCTCTTAT 689
                                                                                                                                                                         ADJ12497 standard; DNA; 24333 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97US-0061463P.
97US-0061527P.
97US-0061529P.
97US-0061532P.
97US-0061536P.
                  3.5%;
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                                                                                                                                                                                                                  (first entry)
                                       58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RUBEN S M.
FLORENCE K A.
GREENE J M.
YOUNG P E.
                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BREWER L A.
DUAN R D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FERRIE A M.
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FLORENCE C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ROSEN C A.
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OLSEN H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-OCT-1997;
09-OCT-1997;
09-OCT-1997;
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                                                                                                                                                                                              ADJ12497;
                    Query Match
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(GREE/)
(YOUN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ROSE/)
                                                                                                                                                             (DUAN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (RUBE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (FERR/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BREW/)
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                                        Matches
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This invanion relates to novel polymucleotides encombinant and synthetic methods for producing human polymucleotides, polypeptides and antibodies. Purthermore, it relates to screening methods to identify agonists and antibodies. Purthermore, it relates to screening methods to identify agonists and antagonists that can be used to inhibit or enhance the production and function of the secreted proteins. The present invention describes these compositions as useful for diagnosing, treating or proventing disorders such as cancer, hematopoletic diseases including anaemia and multiple myeloma, reproductive system disorders including prostatitis and inguinal hernia, musculoskeletal diseases including carpythmia and hypernatraemia, mixed fetal diseases including fetal alcohol syndrome and bown's syndrome, excretory disease including carpythmia and hypernatraemia, mixed fetal diseases including fetal alcohol syndrome and occupational lung disease, endocrine diseases including Alzheimer's disease and meningitis, respiratory disease.

Curinary incontinence and renal disorders, neural or sensory disease.

Curinary incontinence and renal disorders, neural or sensory disease.

Curinary incontinence and renal disorders, neural or sensory disease.

Curinary incontinence and renal disorders, neural or sensory disease.

Curinary incontinence and renal disorders, neural or sensory disease.

Curinary incontinence and renal disorders, neural or sensory disease.

Curinary incontinence and renal disorders, neural or sensory disease.

Curinary incontinence and renal disorders, neural or sensory disease.

Curinary incontinence and renal disorders, neural or secopathic, antisthmatic, antisthmati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8843 caacacceaaacrecreceeerggeragarggaagaargaagcaaaccaaccrrrgerg 8784
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       239 TGCCACCAACTCCAAACCGACAACCCTGTATCTGAGCATGCCTCATGCCTCTCCTTCATG 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention relates to novel polynucleotides encoding human secreted
                                                                                                                                                                                                                                               New isolated nucleic acids and polypeptides, useful for diagnosing, treating, preventing or ameliorating diseases or disorders e.g. cancer, anemia, arthritis, asthma, inflammatory bowel disease or Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
     Greene JM;
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55.2%; Pred. No. 2.3;
tive 0; Mismatches 60; Indels 0;
                                                   Olsen H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human; secreted; cancer; haematopoietic disease; anaemia;
     Florence KA,
Duan RD, Ruben SM, Florence
Yu G, Florence C, Ebner R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 351; 286pp; English.
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ID ADJ12606 Btandard; DNA; 24333 BP.
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Matches 74; Conservative
          Brewer LA,
Ferrie AM,
                                                                                                                                                      WPI; 2004-090518/09.
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inguinal hernia; musculoskeletal disease; systemic lupus erythematosus;

gout; carddovascular disease; arrhythmia; hypernatraemia; fetal disease;

gout; carddovascular disease; arrhythmia; hypernatraemia; fetal disease;

w fetal alcohol syndrome; Down's syndrome; excretory disease;

nurinary incontinence; renal disorder; neural; sensory disease;

Alzheimer's disease; meningitis; respiratory disease; emphysema;

cocupational lung disease; endocrine disease; emphysema;

glomerulonephritis; disease; endocrine disease; scleroderma;

rritable bowel syndrome; epithelial disease; scleroderma;

nritable bowel syndrome; epithelial disease; scleroderma;

mitiaschmacic; antibacterial; osteopathic; dermatological; antigout;

nmitiaschmacic; antibacterial; osteopathic; dermatological; antilipemic;

mingunomodulator; antiarrhythmic; cardiant; noctropic; antilipemic;

methrotropic; uropathic; neuroprocective; antiparkinsonian; tranquilizer;

mutidiabetic; anabolic; hypertensive; vulnerary; ds. multiple myeloma; reproductive system disorder; prostatitis;

Homo sapiens.

JS2004010132-A1.

15-JAN-2004

97US-0061527P. 97US-0061529P. 97US-0061532P. 97US-0061536P. 97US-0071498P. 98WO-US021142. 97US-0061463P 2000US-0244591P 30-OCT-2001; 2001US-00984429 99US-00288143 08-OCT-1998; 08-APR-1999 09-OCT-1997 09-OCT-1997 09-OCT-1997 09-OCT-1997 09-0CT-1997 09-OCT-1997

FLORENCE K A. GREENE J M. YOUNG P E. FERRIE A M. FLORENCE C. EBNER R. OLSEN H. BREWER L A. DUAN R D. RUBEN S M. ROSEN C A. (FLOR/) (EBNE/) (OLSE/) (BREW/) (DUAN/) (RUBE/) (FLOR/) YOUN/) (FERR/) (YUGG/) (ROSE/)

Florence KA, Greene JM; Ebner R, Olsen H; Duan RD, Ruben SM, Yu G, Florence C, Brewer LA, Ferrie AM, Rosen CA, Young PE, Young

WPI; 2004-090518/09.

New isolated nucleic acids and polypeptides, useful for diagnosing, treating, preventing or ameliorating diseases or disorders e.g. cancer, anemia, arthritis, asthma, inflammatory bowel disease or Alzheimer's disease.

Disclosure; SEQ ID NO 460; 286pp; English.

This invention relates to novel polynucleotides encoding human secreted and synthetic methods for producing human polynucleotides, polypeptides and synthetic methods for producing human polynucleotides, polypeptides and antibodies. Furthermore, it relates to screening methods to identify agonists and antagonists that can be used to inhibit or enhance the production and function of the secreted proteins. The present invention describes these compositions as useful for diagnosing, treating or preventing disorders such as cancer, haematopoietic diseases including prostatitis and multiple myeloma, reproductive system disorders including prostatitis and inguinal hernia, musculoskeletal diseases including systemic lupus erythematosus and gout, cardiovascular disease including arrhythmia and hypernatraemia, mixed fetal diseases including alcohol syndrome and Down's syndrome, excretory diseases including urinary incontinence and renal disorders, neural or sensory disease

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including Alzheimer's disease and meningitis, respiratory disease including emphysema and occupational lung disease, endocrine diseases including diabetes and glomerulonephritis, digestive diseases including portal hypertension and irriteable bowel syndrome and connective tissue or epithelial diseases including scleroderma and epidermolysis bullosa. As such, there are various activities such as extostatic, antianemic, antianteric, antiasthmatic, anti-HIV, immunosuppressive, antianemic, antibacterial, osteopathic, dermatclogical, antigout, immunomodulator, antiarrythmic, cardiant, noctropic, antilpemic, nephroropic, antidiabetic, anabolic, hypertensive and vulnerary. This polymucleotide is a DNA fragment of a BAC clone that encodes a human secreted protein of the invention. NOTE: This sequence doces not appear in the printed specification but has been obtained in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        239 TGCCACCAACTCCAAACCGACAACCCTGTATCTGAGCATGCCTCATGCCTCTCCTTCATG 298
                                                                                                                                                                                                                                                                                                                                                                  electronic format from the US patent office at the following web site www.seqdata.uspto.gov/sequence.html; Document ID: 20040010132.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 24333 BP; 6183 A; 6524 C; 6176 G; 5450 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 12; Length 24333;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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ABX14763 standard; DNA; 88191 BP. ABX14763

(first entry) 01-APR-2003 ABX14763;

Genomic DNA encoding novel human ras-like protein.

Ras-like protein; pharmacogenomic analysis; tissue typing; human; transgenic; ribozyme design; gene therapy; alternative splice form; gene;

Homo sapiens.

US2002132291-A1.

19-SEP-2002

07-MAR-2001; 2001US-00799799 (YEJJ/)

07-MAR-2001; 2001US-00799799.

YE J. KETCHUM K A. DI FRANCESCO V. BEASLEY E M. (BEAS/)

(KEIC/)

Di Francesco V, Beasley EM; Ketchum KA, ſе J,

WPI; 2003-174080/17. P-PSDB; ABG72926.

Novel isolated human Ras-like protein useful for treating disorders characterized by absence of, inappropriate or unwanted expression of Ras-like protein, and as immunogens to raise antibodies.

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29-MAY-2003.
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                                          The invention describes an isolated movel human Ras-like polypeptide (I).

The polypeptide is useful for identifying a modulator of (I), by

CC contacting (I) (I), or the nucleotide (I) encoding it, are useful as

CC adeals for the development of human therapeutics, for identifying

CC therapeutic proteins, and as targets for development of human therapeutic

CC degents. (I) is useful as a reagent in assays designed to quantitatively

CC tissues in which the corresponding protein is preferentially expressed,

CC tissues in which the corresponding protein is preferentially expressed,

CC in drug screening assays, to identify compounds that modulate human Ras-

CI ike protein, or an altered form that causes the specific disease or

pathology associated with the protein, to screen a compound for the

CC abhlity to stimulate or inhibit interaction between the Ras-like protein,

CC abhlity to stimulate or inhibit interaction between the Ras-like protein,

CC abhlity to stimulate or inhibit interaction a disorder characterised by

Altered expression of the human Ras-like protein. (II) is useful to

detect the presence of (I) in cells or tissues, to assess abnormal tissue

CC detect the presence of (I) in cells or tissues, to assess anormal tissue

CC detect the presence of (I) in cells or tissues to abnormal expression

during development or progression of a biological condition, to assess

CC normal in pharmacogenomic analysis, for tissue tryping, as diagnostic

C tools, and for inhibiting a protein function. (III) is for expressing

C recombinant vectors, host cells and transgenic animals, for expressing

Thormal and particular the affertivenes of the human Ras-like proteins, for designing

C the contractions of the human Ras-like proteins, for designing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18903 GCGCCCGGCCTCCTTCTGTTTAAGGCTGAACATGATTCTGTTCTATGGAGAGGCCACCTT 18962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140 GCGCGCGCAGCTCCCCCGAGTTTGAGCCGCAATTTTTTACATTTTATGGCGATGGCGTCAG 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene expression. This sequence encodes a novel alternative splice
                                                                                                                                                                                                                                                                                                                                                                                                                                          ribozymes, for monitoring the effectiveness of modulating compounds on the expression or activity of the human Ras-like gene, and for gene therapy in patients containing cells that are aberrant in human Ras-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 88191 BP; 11513 A; 13203 C; 13500 G; 13578 T; 0 U; 36397 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plant; bacterial infection; fungal infection; viral infection; rice; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glazebrook J, Goff SA, Hou Y;
Whitham S, Xie Z, Zhu T, Zou G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 3.3%; Score 37.2; DB 8; Length 88191; 1 Similarity 59.4%; Pred. No. 9; 63; Conservative 0; Mismatches 43; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18963 TICTITATCCAGGITICTAGGAACACTTGAGGGCTTCCACC 19008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  200 GCGTTTATCTAGGCGTCTGGGAGGGTACATTTGAAGATGTGCCACC 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SYGN ) SYNGENTA PARTICIPATIONS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADA71938 standard; DNA; 2000 BP
                  Claim 4; Fig 3; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      form of human ras-like protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cooper B,
S, Tao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-JUN-2001; 2001WO-IB001105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-JUN-2001; 2001WO-IB001105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rice gene, SEQ ID 5263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chang H, Chen W, Co
Katagiri F, Quan S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 63; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO2003000898-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-NOV-2003
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involved in plant resistance or response to pathogenic infection. Mill comprises identifying a gene whose expression is significantly altered in the incomparatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAATTTATCTTTGGGGAGGCGGGCCGGGATTGGAGACAGAGCCCACAAGGCAACAAA 1060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         371 RRRRWAKKSSRTSRRKKRKKWCMRKRKYKRMRGYSRMRSCKRARMMKRCRSGRAWKMGCRG 430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               881
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                                                                                                              Identifying at least one gene involved in plant resistance or response (pathogenic infection for conferring resistance or tolerance to a plant (bacterial, fungal or viral infection by determining or detecting plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | | | : : | : : : : : : : | | : : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a method (M1) for identifying genes
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Best Local Similarity 10.0%; Pred. No. 1.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     English.
                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 27; SEQ ID NO 5263; 899pp;
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2003-175290/17
                                                                                                                                                                                                                                                                                                                gene expression.
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Moughamer T; Ricke D;

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This invention, in the area of plant biotechnology, relates to novel polynucleotides comprising a nucleotide sequence encoding a protein which is involved in or associated with the synthesis, metabolism or carbohydrates in the plant grain and the expression of which is up-regulated during grain filling. The plant is selected from corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco, sugarbeet, wheat, and rice. The invention may be useful for the improvement of protein, oil, starch, fibre and moisture content of the cereal grains. In addition, carbohydrate levels may be modified to a more desirable level using the present invention. The present sequence is a DNA sequence of a rice gene promoter. Note: The sequence data for this peter did not form part of the printed specification, but was obtained fire.wipo.int/pub/publishedpct_sequences.
                                                                                                                                                  New plant genes encoding polypeptides having an activity involved in or associated with the synthesis, metabolism or degradation of carbohydrates in the plant grain useful in generating plants having improved nutritional properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transposable element; rice; mPing/Pong; transposase; transgenic; plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               112 CAGCTTAGGGCAAGTACAATAAGGACTAATCAACCTACTATTAGCCCGTCCAGGTCATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       344 CCGTTTAGAGCAAGTATAATAAGTCCTAGTCAGCTGGCTATAAGATGTTCCACATCAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2000 BP; 480 A; 520 C; 441 G; 559 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 36.2; DB 10;
Pred. No. 2.1;
0; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eddy SR;
                                     , Goff SA,
Provart N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                404 AATCCTTAAACTGGAGGAGAAAGAAAGTAGGAG 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21
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                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 719; 130pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pong-like transposase element; PTE; ds
                                          Cooper B,
Kreps J, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rice PONG_LIKE_2 DNA sequence SeqID
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(SYGN ) SYNGENTA PARTICIPATIONS AG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.3%;
Local Similarity 68.8%;
les 64; Conservative
                                          Zhu T, Cheng W, Briggs S,
Glazebrook J, Katagiri F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-MAR-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-022658/02.
                                                                                                              WPI; 2003-229341/22.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated polypeptide (I) associated with breast cancer which is encoded by a nucleic acid molecule comprising a nucleotide sequence (SI). Further disclosed is an antibody that binds to the polypeptide of the invention. The activity of the polypeptide of the invention as early a sample. Nucleic acid molecules of the invention are useful in the detection of breast tumours. (I) is useful for a marker for breast cancer and in breast cancer therapy. Sequences given in records ACNY8851-ACN92934 represent mucleic acid markers associated with breast cancer. Note: The sequence listing does not form part of the specification but may be obtained in electronic format from the USPTO web site at seqdata.uspto.gov/sequence.thml?DocID=20030099974
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;
carbohydrate degradation; carbohydrate; plant grain; grain filling; corn;
tomato; banana; canola; cotton; peanut; sordhum; tobacco; sugarbeet;
wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32 decaderceacadaaardesecereacidaerdeerrereeagerarereageagea 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                  Novel isolated polypeptide associated with breast cancer, useful for detecting presence of polypeptide in sample, as a marker for breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1023 GCCGGGATTGGAGACAGAGCCCACAAGGCAACAACAAAGTGCGCGTGAGAAAT 1075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92 ATGGGAGTGGGAAATGGAGTACTCAAGGCCACAAGACAGGCCGCCATAGAACT 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.3%; Score 36.2; DB 11; Length 1898; 57.5%; Pred. No. 2; ve 0; Mismatches 48; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1898 BP; 448 A; 416 C; 492 G; 538 T; 0 U; 4 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rice DNA sequence Seq ID719 related to grain filling.
                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 12351; 36pp; English
                                                                                                                                                                봈
                                                                                                                                                                Steinmann
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26-SEP-2001; 2001US-0325277P.
20-DEC-2001; 2001US-0342327P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADC08414 standard; DNA; 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57.5%;
                            18-JUL-2002; 2002US-00198846.
                                                                         18-JUL-2001; 2001US-0306220P.
                                                                                                                 (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                             Wang
                                                                                                                                                                                                          WPI; 2003-787014/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                Lillie J,
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Matches

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RESULT 14 ADC08414/

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1; Gaps

Indels

Length 2000;

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New transposable element comprising at least a portion of a nucleic acid comprising two terminal inverted repeat nucleic acid sequences, useful in designing oligonucleotide primers.
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Claim 6; SEQ ID NO 17; 202pp; English.

and the encoded proteins thereof. Specifically, it refers to the polynucleotides of the mping/Pong family of transposable elements that each comprise two terminal inverted repeat nucleic acid sequences, where the transposable element is actively transposance, these polynucleotides encode proteins that can function as transposaces or proteins that interact with transposaces to meduate transposation of members of the mping/Pong genus. The present invention describes transposation of members of the mping/Pong genus. The present invention describes transposable element is useful for designing oligonucleotide primers that can be used, in turn, for the isolation of related members of the mping/Pong family of transposable elements, and for detecting transpositions of the transposable element. This polynucleotide is the DNA sequence of a member of the rice mping/Pong family, in an This invention relates to novel isolated transposable elements from rice

Sequence 5955 BP; 1788 A; 1252 C; 1123 G; 1792 T; 0 U; 0 Other;

366 GTCCTAGTCAGCTGCTATAAGATGTTCCACATCAGCAAATCCTTAAACTGGAGGAGAAA 425 0; Gaps Query Match
Best Local Similarity 59.0%; Pred. No. 4;
Matches 62; Conservative 0; Mismatches 43; Indels 0; ò

d d

GAAAGTAGGAGTGAGAAGGGCGTCGGCGCTTCGTCAATCGCTAGC 470 426 ઠે

Search completed: August 30, 2005, 13:50:38 Job time : 702 secs

us-09-979-549-2.rni

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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nucleic search, using sw model OM nucleic

Run on:

August 30, 2005, 13:00:09; Search time 228 Seconds (without alignments) 7973.261 Million cell updates/sec

US-09-979-549-2 1111 Title: Perfect score:

1 gaagtcagaaggccgttcag......... Sequence:

Scoring table:

IDENTITY_NUC Gapopt 10.0

1202784 segs, 818138359 residues Searched:

2405568 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued Patents_NA:*

'GgDZ_6/ptodata1/ina/5A_COMB.seq:*
'GgDZ_6/ptodata1/ina/6A_COMB.seq:*
'GgDZ_6/ptodata1/ina/6A_COMB.seq:*
'GgDZ_6/ptodata1/ina/6B_COMB.seq:*
'GgDZ_6/ptodata1/ina/BCGOMB.seq:*
'GgDZ_6/ptodata1/ina/PCTUS_COMB.seq:*
'GgDZ_6/ptodata1/ina/backfiles1.seq:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

		*			SUMMARIES	
Result No.	Score	Query	Query Match Length	BB	ΙD	Description
1	39.8	3.6	38503	4	US-09-949-016-17257	Sequence 17257, A
~	39.8	3.6	39715	4	US-09-949-016-12454	
m	39.2	3.5	601	4	US-09-949-016-170604	Sequence 170604,
4	38	3.4	27465	4	US-09-949-016-16561	Sequence 16561, A
υ S	37.6	3.4	832	4	US-09-621-976-2813	
9 U	37.2	3.3	601	4	US-09-949-016-31783	
7	37.2	3.3	601	4	US-09-949-016-193904	
œ U	37	3.3	289	m	US-09-007-005-17	17,
O O	37	3.3	289	m	US-09-244-796-17	
10	36.2	3.3	53915	4	US-09-949-016-12221	1222
11	36.2	3.3	53915	4	US-09-949-016-12730	Sequence 12730, A
12	36.2	3.3	53924	4	US-09-949-016-12947	12947,
13	36.2	3.3	53924	4	US-09-949-016-12948	12948,
14	35.8	3.5	460	4	US-09-513-999C-32264	322(
15	35.2	3.2	1141	4	US-09-806-708B-22	
16	35	3.2	27968	4	US-09-949-016-15191	151
17	35	3.2	27968	4	US-09-949-016-15192	151
	35	3.2	108310	4	US-09-949-016-16366	Sequence 16366, A
c 19	34.8	3.1	541	4	US-09-270-767-10710	10710,
c 20	34.2	3.1	11740	4	US-09-949-016-13670	Sequence 13670, A
c 21	33.8	3.0	56832	4	US-09-949-016-12976	12
22	33	3.0	168575	m	US-09-426-290-1	
23	32.6	2.9	601	4	US-09-949-016-57820	57
c 24	32.6	2.9	12603	4	US-09-949-016-17096	
25	32.6	2.9	20495	4	US-09-949-016-17198	17198
26	32.6	2.9	42988	4	US-08-311-731A-128	Sequence 128, App
27	32.6	2.9	134292	4	US-09-949-016-12158	Sequence 12158, A

21113 CAGGCAT 21119

C 29 32.6 2.9 236474 4 US-09-949-016-13418 C 30 32.4 2.9 1128 4 US-09-54-236-165 C 31 31.8 2.9 7218 1 US-08-232-463-11 C 32 31.8 2.9 16044 4 US-09-949-016-16378 33 31.8 2.9 16044 4 US-09-949-016-17027 34 31.8 2.9 147840 4 US-09-949-016-15236 35 31.6 2.8 3893 4 US-09-949-016-15336 38 31.6 2.8 41199 4 US-09-949-016-15306 39 31.6 2.8 84296 4 US-09-949-016-17029 40 31.4 2.8 14296 4 US-09-949-016-17375 41 31.4 2.8 14464 4 US-09-583-110-591 42 31.4 2.8 14463 4 US-09-107-433-2028 43 31.4 2.8 14463 4 US-09-16-127-8 44 31.4 2.8 105055 4 US-09-949-016-15376 45 31.4 2.8 11443 3 US-08-110-591 45 31.4 2.8 11463 4 US-09-16-1257-8 46 31.4 2.8 105055 4 US-09-949-016-12505	Sequence 13418, A Sequence 165, App	Sequence 11, Appl	Sequence 14, Appl	Seguence 16378, A	Seguence 17027, A	Sequence 15236, A	Sequence 15639, A	Sequence 15700, A	Sequence 17269, A	Sequence 16348, A	Sequence 17375, A	Sequence 8976, Ap	Sequence 591, App	Sequence 2028, Ap	Sequence 49, Appl	Sequence 14001, A	Sequence 12505, A
2 4 1 4 4 4 4 4 8 1 10 10 10 10 10 10 10 10 10 10 10 10 1	US-09-949-016-13418 US-09-540-236-165	US-09-596-002-11	US-08-232-463-14	US-09-949-016-16378	US-09-949-016-17027	US-09-949-016-15236	US-09-621-976-15639	US-09-949-016-15700	US-09-949-016-17269	US-09-949-016-16348	US-09-949-016-17375	US-09-621-976-8976	US-09-583-110-591	US-09-107-433-2028	US-08-961-527-49	US-09-949-016-14001	US-09-949-016-12505
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ALIGNMENTS

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Sequence 17257, Application US/09949016

Sequence 17257, Application US/09949016

Patent No. 681239

GENERAL INFORMATION:

TOTAGE OF INVENTION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 00/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FRESE FASTESEQ for Windows Version 4.0

SEQ ID NO 17257

LEWARTH: 38503
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Best Local Similarity 50.8%; Pred. No. 0.14;
Matches 95; Conservative 0; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LOCATION: (1) ... (36503); OTHER INFORMATION: n = A,T,C or G US-09-949-016-17257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
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US-09-949-016-17257
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Matches
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOOLAGY
CURRENT APPLICATION NUMBER: 06/241,755
FRIOR PILING DATE: 2000-04-14
PRIOR PILING DATE: 2000-10-20
FRIOR PELING DATE: 2000-10-03
FRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTESE for Windows Version 4.0
ENGINENT: 39715
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0
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Pred. No. 0.14;
0; Mismatches 92; Indels 0;
                               ; Sequence 12454, Application US/09949016; Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION: (1)...(39715)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 50.8'
Matches 95; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature
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ORGANISM: Human
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ORGANISM: Human
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FACELIA NO. 1915.37
FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: 06/241,755
FRIOR APPLICATION NUMBER: 66/241,755
FRIOR FILING DATE: 2000-10-20
FRIOR FILING DATE: 2000-10-3
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FREESEQ for Windows Version 4.0
LENGTH: 27465
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                                                                                                                                                                                                                                                     282 CAACACCAAACTCCTCCCRCCTGGCTAGATGGGGAGCATGGAGCAACCAACCTTGCTG 341
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                                                                                                       179 ATTITATGGCGATGGCGTCAGGCGTTTATCTAGGCGTCTGGGAGGGTACATTTGAAGATG
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     Length 601;
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Score 39.2; DB 4; Length 6 Pred. No. 0.014; 1; Mismatches 59; Indels
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Sequence 2813.74/2015
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dunes Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REPERENCE: GENEET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
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                                                            Conservative
                        Local Similarity
nes 74; Conserv
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US-09-949-016-16561
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193 GCGTCAGGCGTTTATCTAGGCGTCTGGGAGGGTACATTTGAAGATGTGCCACCAACTCCA 252
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                                                                                                                                  42 Accrecercecegerrecadesarrerecidecreager 1
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CURRENT FILING DATE: 1998-01-14
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1997-01-27
EARLIER FILING DATE: 1997-01-27
EARLIER FILING DATE: 1997-11-06
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 289
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; Sequence 193904, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
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Best Local Similarity 51.9%;
Matches 84; Conservative (
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; ORGANISM: Human
US-09-949-016-193904
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US-09-007-005-17/c
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US-09-949-016-31783/c

Sequence 31783, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOO1307

CURRENT PILING DATE: 2000-04-14

PRIOR PELLING DATE: 2000-04-14

PRIOR PELLING DATE: 2000-10-20

PRIOR PAPLICATION NUMBER: 60/237,768

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

NUMBER OF SEQ ID NOS: 207012

SOCTHARRE: PSELSEQ for Windows Version 4.0

SEG ID NO 31783

LENGTH: 601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      318 RKYTWGWWYWWKRMMSTRWYCYMCWKCCMYRGRRCAWYTMARGRMWSYAWGKWKSMRSA 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  258 MSMCTRMYYKKGSTYWTWKCTCATWCYWYWKYWKRWWSKTCWSGSRGGYMTSYTSTRSYS 199
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                                                                                                                                                                                                                                                      Query Match 3.4%; Score 37.6; DB 4; Length 832; Best Local Similarity 11.6%; Pred. No. 0.062; Matches 40; Conservative 150; Mismatches 154; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78 AMAYGKTMIMIRACWKTRYWRWWAWAMWRMWTMIMIMIYYWYWRAM 35
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 2813
                                                                                         TYPE: DNA ORGANISM: Homo sapiens
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es 84; Conserv
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, LOCATION: 235..399
US-09-621-976-2813
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US-09-949-016-31783
                                                                   LENGTH: 832
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Best Local S:
Matches 84
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
FRIOR PELICATION NUMBER: 60/231,756
FRIOR PELICATION NUMBER: 60/231,768
FRIOR PELICATION NUMBER: 60/231,498
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NO 193904
LENGTH: 601 193 GCGTCAGGCGTTTATCTAGGCGTCTGGGAGGGTACATTTGAAGATGTGCCACCAACTCCA 252 102 gagiticgcicticitgirecccagecresasiesanisecaccarcicagireaceca 43 102 GAGTITICGCTCTTGTTGCCCCAGGCTGGAGTGCAATGGCACCATCTCAGTTCACCGCA 43 133 TGGGTGGGCGCGCGCGCGCCCCGAGTTTGAGCCGCAATTTTTTACATTTTATGGCGATG 162 raggrereagecacrecaccedecerragaagecaárrirrrrrrrrrragagare . 0 Sequence 17, Application US/09007005B
Patent No. 6258558
GENERAL INFORMATION:
APPLICANT: Scoatsk, Jack W.
APPLICANT: Roberts, Richard W.
APPLICANT: Liu, Rihe
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
FITLE OF INVENTION: FUSIONS
FILE REFERENCE: 00786/350003 Score 37.2; DB 4; Length 6 Pred. No. 0.068; 0; Mismatches 78; Indels

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154 NYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNY
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NAME/KEY: misc feature
LOCATION: (1)...(53915)
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ORGANISM: Human
                                                                  RESULT 10
US-09-949-016-12221
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LENGTH: 53915
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                                                                                                                                                                                                                                                                                                170 TTTTTTACATTTTAIGGCGAIGGCGTCAGGCGTTTATCTAGGCGTCTGGGAGGGTACAT 229
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Sequence 17, Application US/09244796

Patent No. 6281344

GENERAL INFORMATION:

APPLICANT: Scottak, Jack W.

APPLICANT: Liu, Rihe

TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN

TITLE OF INVENTION: EUS.003

FILE REFERENCE: 00786/350007

CURRENT PAPLICATION NUMBER: US/09/244,796

CURRENT APPLICATION NUMBER: 60/035,963

EARLIER APPLICATION NUMBER: 60/044,91

EARLIER FILING DATE: 1997-01-27

EARLIER FILING DATE: 1997-01-27

EARLIER FILING DATE: 1997-01-27

EARLIER FILING DATE: 1997-01-27

EARLIER FILING DATE: 1998-01-14

NUMBER OF SEQ ID NOS: 33

NUMBER OF SEQ ID NOS: 33

NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                                                         3.3%; Score 37; DB 3; Length 289; 10.6%; Pred. No. 0.049;
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                                                                                                                                                                                                                                                   86; Indels
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                                                                                                                                                                                                                                                 75; Mismatches
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                                            OTHER INFORMATION: Translation template
                                                             FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(289)

OTHER INFORMATION: n = A,T,C or G
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; OTHER INFORMATION: n = A,T,C or G
US-09-244-796-17
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                   Conservative
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Best Local Similarity
Matches 19; Conserva
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LENGTH: 289
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APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOOI 307

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR PILING DATE: 2000-04-14

PRIOR PILING DATE: 2000-10-20

PRIOR PLILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-09

NUMBER: OS/231,498

PRIOR PILING DATE: 2000-09-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48;
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3.3%; Score 36.2; DB 4;
Best Local Similarity 57.5%; Pred. No. 3;
Matches 65; Conservative 0; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 12730, Application US/09949016; Patent No. 6812339; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature
LOCATION: (1).T.(53915)
OTHER INFORMATION: n = A,T,C or G
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OTHER INFORMATION: n = A,T,C or G
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Gaps

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44530 GGGAGTCCACAGAAAATGGGGCCTCACTGACTGCTTGTCCAGGTATCTCAGTGGGAA 44589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | FALENT NO. 6'183961 |
| GENERAL INFORMATION: BAWARDEN J.B. |
| APPLICANT: Duclert, A. |
| APPLICANT: Duclert, A. |
| APPLICANT: Duclert, A. |
| APPLICANT: Giordano, J.Y. |
| TITLE OP INVENTION: Expressed Sequence Tags and Encoded Human Proteins. |
| PILE REFERENCE: 59.US2.REG |
| FILE REFERENCE: 59.US2.REG |
| CURRENT FILING DATE: 2000-02-24 |
| PRIOR APPLICATION NUMBER: US 60/122,487 |
| PRIOR PLING DATE: 1999-02-26 |
| NUMBER OF SEQ ID NOS: 36681 |
| SOFTWARE: PARENT. PM |
| SOFTWARE: PARENT. PM |
| SOFTWARE: PARENT. |
| LENGTH: 460 |
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                                                                                                                                                                                                                                                                                                          Query Match 3.3%; Score 36.2; DB 4; Length 53924; Best Local Similarity 57.5%; Pred. No. 3; Matches 65; Conservative 0; Mismatches 48; Indels 0;
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12948
LENGTH: 53924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 32264, Application US/09513999C Patent No. 6783961
                                                                                              TYPE: DNA
CRGANISM: Human
FEATURE:
NAME/KEY: mlsc_feature
LOCATION: (1)...(53924)
CTHER INFORMATION: n = A,T,C or G
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LOCATION: 26
OTHER INFORMATION: s=g or c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 193 TOTHER INFORMATION: m=a or c
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NAME/KEY: misc_feature
LOCATION: 188
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NAME/KEY: misc_feature
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ORGANISM: Homo sapiens
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LOCATION: 311
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LOCATION: 353
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APPLICATE: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REPERRUCE: CLOO1307;
CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,756
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PELING DATE: 2000-10-03
PRIOR PELING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NO 12947

LENGTH: 53924
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: 05/0949,016
RIOR APPLICATION NUMBER: 05/241,755
RRIOR APPLICATION NUMBER: 60/241,756
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-0
                                                                                                                                                                              963 GCGAGCGCATAAATTCTGATTCCTGCCTGCCTGCCGGACAATTTATCTTTGGGGAGGCGG 1022
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                             Length 53915;
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                          Query Match 3.3%; Score 36.2; DB 4; Length 5 Best Local Similarity 57.5%; Pred. No. 3; Matches 65; Conservative 0; Mismatches 48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 3.3%; Score 36.2; DB 4; Length 5 Best Local Similarity 57.5%; Pred. No. 3; Matches 65; Conservative 0; Mismatches 48; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12947, Application US/09949016; Patent No. 6812339; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | NAME/KEY: misc_feature
| LOCATION: (1)...(53924)
| OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12947
                                                                                                                                                                                                                                                                                                                                                             RESULT 12
US-09-949-016-12947
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
US-09-949-016-12948
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LOCATION: (1)...(1141)
CTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. FAE1 promoters
US-09-806-708B-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    217 TOGGAGGGTACATTTGAAGATGTGCCACCAACTCCAAACCGACAACCTGTATCTGAGCA 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 22, Application US/09806708B

Sequence 22, Application US/09806708B

Patent No. 6784342

GENERAL INFORMATION:
PAPLICANT: The University of British Columbia

TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
FILE REFERENCE: 4810-58741

CURRENT APPLICATION NUMBER: US/09/806,708B

CURRENT APPLICATION NUMBER: US 60/147,133

PRIOR PILING DATE: 1999-08-04

NUMBER OF SEQ ID NOS: 23

SOFTWARE: PatentIn version 3.0

SEQ ID NO 22

LENGTH: 1141
                                                                                                                                                                                                                                                                                                                                                                                                                                          272 gegagrecacagaaangeegeereacreacrescrectionageiarereacrega
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    gor
                                                                                                 FEATURE:

NAME/KEY: misc_feature

LOCATION: 459

OTHER INFORMATION: k=g or t

FEATURE:

NAME/KEY: misc_feature

LOCATION: 460

OTHER INFORMATION: y=c or t

US-09-513-999C-32264
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ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 56.6
Matches 64; Conservative
               FEATURE:
NAME/KEY: misc_feature
LOCATION: 458
OTHER INFORMATION: y=c or
OTHER INFORMATION: d=a or
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US-09-806-708B-22
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1073 AWRWRWGKATCYMTDNA 1089
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Search completed: August 30, 2005, 16:31:26 Job time : 232 secs

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Sequence 15660, A Sequence 9, Appli Sequence 733, Ap Sequence 4, Appli Sequence 6, Appli Sequence 351, App
                                                                                                                                                                            August 30, 2005, 13:39:06; Search time 859 Seconds (without alignments) 8462.599 Million cell updates/sec
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11. (1902 6/ptodata1/pubpna/USO7 PUBCOMB.seq:*

12. (1902 6/ptodata1/pubpna/USO6 NEW PUB.seq:*

13. (1902 6/ptodata1/pubpna/USO6 NEW PUB.seq:*

14. (1902 6/ptodata1/pubpna/USO6 PUBCOMB.seq:*

15. (1902 6/ptodata1/pubpna/USO8 PUBCOMB.seq:*

16. (1902 6/ptodata1/pubpna/USO8 NEW PUB.seq:*

17. (1902 6/ptodata1/pubpna/USO8 PUBCOMB.seq:*

18. (1902 6/ptodata1/pubpna/USO8 PUBCOMB.seq:*

19. (1902 6/ptodata1/pubpna/USO8 PUBCOMB.seq:*

10. (1902 6/ptodata1/pubpna/USO8 PUBCOMB.seq:*

10. (1902 6/ptodata1/pubpna/USO8 PUBCOMB.seq:*

11. (1902 6/ptodata1/pubpna/USO9 PUBCOMB.seq:*

12. (1902 6/ptodata1/pubpna/USO9 NEW PUB.seq:*

13. (1902 6/ptodata1/pubpna/USO9 NEW PUB.seq:*

14. (1902 6/ptodata1/pubpna/USO9 NEW PUB.seq:*

15. (1902 6/ptodata1/pubpna/USO9 PUBCOMB.seq:*

16. (1902 6/ptodata1/pubpna/USO9 PUBCOMB.seq:*

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18. (1902 6/ptodata1/pubpna/USO9 PUBCOMB.seq:*

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10. (1902 6/ptodata1/pubpna/USO9 PUBCOMB.seq:*

11. (1902 6/ptodata1/pubpna/USO9 NEW PUB.seq:*

12. (1902 6/ptodata1/pubpna/USO9 NEW PUB.seq:*

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18. (1902 6/ptodata1/pubpna/USO9 NEW PUB.seq:*

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19. (1902 6/ptodata1/pubpna/USO9 NEW PUB.seq:*
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-10-311-193-9
US-10-260-238-5967
US-10-481-032A-733
US-10-459-262A-4
US-10-415-0586
US-00-984-429-351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7331713 segs, 3271544945 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Published Applications NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                       - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                       IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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Match Length DB
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Perfect score:
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C 8 38 3.4 24333 11 US-09-984-429-460 10 37 3.3 4211 18 US-10-424-599-385 11 36.2 3.3 2000 22 US-10-424-599-385 12 36.2 3.3 2000 22 US-10-424-18601 18 35 3.2 704 20 US-10-563-48A-18602 18 31 3.2 704 20 US-10-563-48A-18602 18 31 3.2 704 20 US-10-563-48A-18602 19 31 8 3.1 704 21 US-10-563-48A-18602 20 31 48 3.1 554 18 US-10-46-731-10 21 34.8 3.1 554 18 US-10-46-731-10 22 34.8 3.1 554 18 US-10-46-731-10 23 34.8 3.1 554 17 US-10-41-756-10 24 34.8 3.1 554 17 US-10-41-756-10 25 34.8 3.1 554 17 US-10-41-756-10 26 34.8 3.1 554 17 US-10-41-756-10 27 34 34 8 3.1 554 17 US-10-41-756-10 28 34 8 3.1 554 17 US-10-41-756-10 29 34 8 3.1 554 17 US-10-41-756-10 29 34 8 3.1 18491 13 US-10-86-448-1176 29 34 8 3.1 18491 13 US-10-86-48-1176 29 34 8 3.1 554 17 US-10-40-86-41-176 20 34 48 3.1 554 17 US-10-41-756-10 21 34 8 3.1 18491 13 US-10-86-48-1176 21 34 8 3.1 18491 13 US-10-86-48-1176 22 34 8 3.1 18491 13 US-10-86-48-1176 23 34 8 3.1 18491 13 US-10-86-48-1176 24 34 8 3.1 18931 13 US-10-86-48-1176 25 34 8 3.1 18931 13 US-10-86-48-1176 26 34 8 3.1 18931 13 US-10-86-48-1176 27 41 34.2 3.1 18931 13 US-10-86-48-1176 28 44 34.2 3.1 18931 13 US-10-86-48-1176 29 44 34.2 3.1 18931 13 US-10-86-48-1176 20 20 20 20 20 20 20 20 20 20 20 20 20 2
38 3.4 24333 37.2 3.3 88191 36.2 3.3 88191 36.2 3.3 1898 36.2 3.3 1898 36.2 3.3 1898 36.2 3.3 2000 36.2 3.3 2000 35.2 3.3 2000 35.2 3.3 2000 35.2 3.3 2000 35.3 3.2 704 34.8 3.1 594 34.8 3.1 594 34.8 3.1 594 34.8 3.1 594 34.8 3.1 594 34.8 3.1 18649 34.8 3.1 18649 34.8 3.1 18649 34.8 3.1 18649 34.8 3.1 18649 34.8 3.1 772 34.8 3.1 18649 34.8 3.1 18649 34.8 3.1 18649 34.8 3.1 18649 34.8 3.1 18649 34.8 3.1 18649 34.8 3.1 18649 34.8 3.1 18649 34.8 3.1 18649 34.8 3.1 18649 34.8 3.1 18649 34.8 3.1 18649 34.8 3.1 18649 34.8 3.1 18649 34.8 3.1 18649 34.8 3.1 18031 34.6 3.1 887 34.6 3.1 887 34.6 3.1 887 34.6 3.1 887 34.6 3.1 887 34.6 3.1 887 34.6 3.1 8649 34.8 3.1 18039 34.2 3.1 18649 34.8 3.1 18039 34.2 3.1 18649 34.8 3.1 18039 34.2 3.1 18649 34.8 3.1 18039 34.2 3.1 18649 34.8 3.1 18931 34.6 3.1 887 34.6 3.1 887 34.6 3.1 887 34.6 3.1 887 34.6 3.1 887 34.6 3.1 887 34.8 3.1 18931 34.6 3.1 887 34.8 3.1 18931 34.8 3.1 18649 34.8 3.1 18931 34.8 3.1 189
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85

9

1008 TCTTTGGGGAGGCGGGCCGGGATTGGAGACAGAGCCCACAAGGCAACAAGTGCGCG 1067

1 TATTTCGGGGGGGGGGGGGGGGGTTCGAGAGCCCACAAGGCAACAACAAAGTGCGCG

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350 AGAGCAAGTATAATAAGTCCTAGTCAGCTGGCTATAAGATGTTCCACATCAGCAAATCCT 409
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4.3%; Score 47.8; DB 21; Length 9538;
Best Local Similarity 62.9%; Pred. No. 0.00057;
Matches 90; Conservative 0; Mismatches 52; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: misc feature
LOCATION: (9471)..(9471)
COTHER INFORMATION: n is a, c, g, or t
US-10-311-193-9
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LOCATION: (9260)...(9260)
OTHER INFORMATION: n is a, c, g, or t
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LOCATION: (6735)..(6735)
OTHER INFORMATION: n is a, c,
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LOCATION: (6675)..(6675)
OTHER INFORMATION: n is a, c,
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OTHER INFORMATION: n is a, c,
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NAME/KEY: misc feature
LOCATION: (7516)..(7516)
OTHER INFORMATION: n is a,
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LOCATION: (9121)..(9121)
OTHER INFORMATION: n is a,
                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (6627)...(6627)
OTHER INFORMATION: n is a,
                                                                                                          NAME/KEY: misc feature
LOCATION: (6619)..(6619)
OTHER INFORMATION: n is a,
                                                                                                                                                                                                                                                       NAME/KEY: misc feature
LOCATION: (6632)..(6632)
OTHER INFORMATION: n is a,
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LOCATION: (6647)..(6647)
OTHER INFORMATION: n is a,
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LOCATION: (6696)..(6696)
OTHER INFORMATION: n is a,
OTHER INFORMATION: n is a,
                     FEATURE:
NAME/KEY: misc_feature
LOCATION: (6536)..(6536)
OTHER INFORMATION: n is
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LOCATION: (9095)..(9095)
OTHER INFORMATION: n is
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APPLICANT: LIDGETT, Angela June
APPLICANT: LIDGETT, Angela June
APPLICANT: LIDGETT, Angela June
APPLICANT: JOHNSON, Xenie Angela
APPLICANT: JOHNSON, Xenie Angela
APPLICANT: JOHNSON, Xenie Angela
TITLE OF INVENTION: FRUCTOSYL TRANSFERASE HOMOLOGUES FROM RYEGRASS (LOLIUM) AND
TITLE OF INVENTION: FRUCTOSYL 18A10/311,193
CURRENT APPLICATION NUMBER: US/10/311,193
CURRENT FILING DATE: 2000-12-13
PRIOR PELICATION NUMBER: PQE155
PRIOR APPLICATION NUMBER: PCT/AU01/00705
PRIOR FILING DATE: 2001-06-14
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn version 3.2
SEQ ID NO 9
LENGTH: 9538
                     61 TGAGA----AACAAGCGGTGCTTGCCGAGAAGAGAGAGAGAGAG 100
                                                                                                                                              Sequence 9, Application US/10311193
Publication No. US20050089845A1
GENERAL INFORMATION:
APPLICANT: SPANGENBERG, German Carlos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: misc_feature
LOCATION: (6404)
OTHER INFORMATION: n is a, c, g, or
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OTHER INFORMATION: n is a, c, g,
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NAME/KEXT: misc_feature
LOCATION: (3698)
OTHER INFORMATION: n is a, c,
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LOCATION: (6221)..(6221)
OTHER INFORMATION: n is a, c,
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LOCATION: (4669)..(4669)
OTHER INFORMATION: n is a, c,
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NAME/KEY: misc feature
LOCATION: (5546)
OTHER INFORMATION: n is a, c,
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LOCATION: (5611)..(5611)
OTHER INFORMATION: n is a, c,
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LOCATION: (6033)..(6033)
OTHER INFORMATION: n is a, c,
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LOCATION: (5615)..(5616)
OTHER INFORMATION: n is a,
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LOCATION: (6528)..(6528)
OTHER INFORMATION: n is a,
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LOCATION: (6533)..(6534)
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NAME/KEY: misc feature
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ORGANISM: Magnaporthe grisea
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Matches 53; Conservative
                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Oryza sativa
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       696 raagagcaagraragraargracagrcagcrgscgaaarcaaccgcrgcgrcarccaaar 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          408 CTTAAACTGGAGGAGAAAGAAAGTAAGGAGTGAGAAGGGCGTCGGCGCTTCGTCAATCGCT 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        636 C-CAACGTGGAGGAGGAAAACCAAGAAAGAAAGAAATGGACGAGTCGCGAGTCGCC 578
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APPLICANT: Frovart, Nicolas
APPLICANT: Ricke, Darrell
TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
FILE REFERENCE: 601480SPCT
CURRENT APPLICATION NUMBER: US/10/481,032A
CURRENT FILING DATE: 2003-12-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Budworth, Paul R.
APPLICANT: Budworth, Paul R.
APPLICANT: Budworth, Bret
APPLICANT: Cooper. Bret
APPLICANT: Cooper. Bret
APPLICANT: Goff, Stephen A.
APPLICANT: Glazebrock, Jane
APPLICANT: Glazebrock, Jane
APPLICANT: Ricke, Darrell
APPLICANT: Ricke, Darrell
APPLICANT: APPLICANT: Ricke, Darrell
APPLICANT: APPLICANT: Shown NUMBER: US/10/260,238
TILE REFERENCE: 60111-NP
FILE REFERENCE: 60111-NP
CURRENT APPLICATION NUMBER: US/020-09-26
PRIOR PLLING DATE: 2001-09-26
PRIOR PLLING DATE: 2002-04-04
NUMBER OF SEQ ID NOS: 6077
SEQ ID NO 5967
LENGTH: 1976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7
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Pred. No. 0.0012;
0; Mismatches 67; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          577 GGCTCGAAGCGTCGTACCCGAGCAAAACGCCCGCTCCCAACTCG 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        468 AGCGATAGCACAAGCTCCCATGGAATCGAGCCAACATGCAACCCG 512
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US-10-481-032A-733/C

Sequence 733, Application US/10481032A

Publication No. US20050177901A1

GENERAL INFORMATION:

APPLICANT: Zhu, Tong

APPLICANT: Cheng, Wengiong

APPLICANT: Cooper, Bret

APPLICANT: Cooper, Bret

APPLICANT: Gooper, Bret

APPLICANT: Gooper, Bret

APPLICANT: Gooper, Bret

APPLICANT: Glaschrook, Jane

APPLICANT: Glaschrook, Jane

APPLICANT: Glaschrook, Jane

APPLICANT: Glaschrook, Jane

APPLICANT: Tong
  8108 CTCTAGCACGTGCTCCTAGGCAA 8130
                                                                    RESULT 3
US-10-260-238-5967/c
US-10-260-238-5967/c
Publication No. US20040016025A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.1%;
Local Similarity 58.8%;
les 97; Conservative 0
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; ORGANISM: Oryza sativa
US-10-260-238-5967
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Matches
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PRIOR PAPILOTON NUMBER 108 60/300,112

PRIOR PLINE DATE: 2001-06-25

PRIOR PLINE DATE: 2001-06-26

PRIOR PAPILOTON NUMBER: 108 60/322,277

PRIOR PAPILOTON NUMBER: 108 60/326,277

PREMIURS: 108 60/326,310

PREMIURS: 108 60/326,320

PREMIURS:
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8903 Archagradadacradadadadadacradadadacrrarrandahadardadard 8844
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            239 TGCCACCAACTCCAAACCGACAACCCTGTATCTGAGCATGCCTCATGCCTCTCCTTCATG 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 38; DB 11; Length 24333;
Pred. No. 1.8;
0; Mismatches 60; Indels 0
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Publication No. US20040010132A1

GENERAL INFORMATION: 53 Human Secreted Proteins
FILE REFRENCE: PSO18P2

CURRENT APPLICATION NUMBER: US/09/984,429

CURRENT PILING DATE: 2001-10-30

PRIOR APPLICATION NUMBER: 09/288,143

PRIOR APPLICATION NUMBER: 09/288,143

PRIOR FILING DATE: 1999-0-08

PRIOR FILING DATE: 1998-10-08

PRIOR FILING DATE: 1998-10-09

PRIOR FILING DATE: 1997-10-09

PRIOR PRIOR APPLICATION NUMBER: 60/061,529

PRIOR PRIOR APPLICATION NUMBER: 60/061,529

PRIOR PRIOR APPLICATION NUMBER: 60/061,529

PRIOR PRILING DATE: 1997-10-09

PRIOR FILING DATE: 1997-10-09

PRIOR FILING DATE: 1997-10-09

PRIOR PRILING DATE: 1997-10-09

PRIOR FILING DATE: 1997-10-09

PRIOR PRIOR FILING DATE: 1997-10-09
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                   PRIOR APPLICATION NUMBER: 60/061,529
PRIOR FILING DATE: 1997-10-09
PRIOR FILING DATE: 1997-10-09
PRIOR PILING DATE: 1997-10-09
PRIOR PILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/061,527
PRIOR APPLICATION NUMBER: 60/061,536
PRIOR APPLICATION NUMBER: 60/061,536
PRIOR PILING DATE: 1997-10-09
PRIOR PILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 727
SOFTWARE: PATENTING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 727
SOFTWARE: PATENTING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 727
SOFTWARE: PATENTING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 727
LENGTH: 24333
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Best Local Similarity 55.2%;
Matches 74; Conservative
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US-09-984-429-351
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US-09-984-429-460/c
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Sequence 6, Application US/10415058

Publication No. US200400600B1A1

GENERAL INFORMATION:
APPLICANT: Wisconsin Alumni Research Foundation
APPLICANT: United States Department Of Agriculture
APPLICANT: Leong, Sally A.
APPLICANT: Leong, Sally A.
APPLICANT: Chauhan, Railnder
APPLICANT: Soloron
APPLICANT: Chauhan, Railnder
APPLICANT: Soloron
APPLICANT: Chauhan, Railnder
APPLICANT: Soloron
APPLICANT: Chauhan, Railnder
APPLICANTON NUMBER: USN 60/242,313
PRIOR APPLICATION NUMBER: USN 60/242,313
PRIOR APPLICATION NUMBER: USN 60/303,897
PRIOR APPLICATION NUMBER: USN 60/303,897
PRIOR PILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.1
SEQ ID NOS: 14
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                                                                         601 CAGCCAGTTTATTATATAAACAGGCTATATAGCTGACCTGGCAGTGCTATAGAGCCGGCA 660
   Gaps
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31; Indels
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US-09-984-429-531/C
Publication No. US20040010132A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: 53 Human Secreted Proteins
FILE REPERENCE: P5018P2
CURRENT APPLICATION NUMBER: US/09/984,429
CURRENT FILING DATE: 2001-10-30
FRIOR APPLICATION NUMBER: 60/244,591
FRIOR APPLICATION NUMBER: 09/288,143
FRIOR FILING DATE: 1999-04-08
FRIOR FILING DATE: 1999-04-08
FRIOR FILING DATE: 1999-10-08
FRIOR FILING DATE: 1999-10-08
FRIOR FILING DATE: 1999-10-08
FRIOR FILING DATE: 1998-10-08
FRIOR APPLICATION NUMBER: 60/061,463
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       0; Mismatches
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LOCATION: (26297)..(26395)
OTHER INFORMATION: N is any nucleotide
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Matches 58; Conservative
       58; Conservative
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ORGANISM: Oryza Bativa
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       Matches
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NAME/KEY: unsure
LOCATION: (1)..(421)
OCHER INFORMATION: unsure at all n locations
FEATURE:
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US-10-481-032A-719/c
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Best Local S
Matches 76
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPREBUCE 38-21(5223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18903 GCGCCCGGCCTCCTTCTGTTTAAGGCTGAACATGATTCTGTTCTATGGAGAGGCCACCTT 18962
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                                                                                                    3903 Arcregregegerregreacaegecrerereresagaegaerrereagaagareagaagare 8844
                                                                                                                                                                                     8843 caacaccaaacrecréececeresérasáressasearesaséaaccaaccriresre 8784
                                                               179 ATTTTATGGCGATGGCGTCAGGCGTTTATCTAGGCGTCTGGGAGGGTACATTTGAAGATG 238
                                                                                                                                              239 TGCCACCAACTCCAAACCGACAACCCTGTATCTGAGCATGCCTCATGCCTCTCCTTCATG 298
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                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:

APPLICANT: YE, Jane et al.

TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE

TITLE OF INVENTION: PROTEINS, AND USES THEREOF

FILE REFERENCE: CLOO1157

CURRENT RELING DATE: 2001-03-07

NUMBER OF SEQ ID NOS: 5

SOFTWARE: FastSEQ for Windows Version 4.0

ELNGTH: 88191
                        Gaps
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                     60; Indels
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Pred. No. 6.7;
0; Mismatches
55.2%; Pred. No. 1.8; tive 0; Mismatches

; LOCATION: (1)...(88191)
; OTHER INFORMATION: n = A,T,C or G
US-09-799-799-3
                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/09799799; Patent No. US20020132291A1
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Best Local Similarity 59.4%;
Matches 63; Conservative (
                                                                                                                                                                                                                                                                          8783 CCTGCTGTGGGGTG 8770
                                                                                                                                                                                                                                   CCTCCCTTTGGGTG 312
                     74; Conservative
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ORGANISM: Glycine max
FEATURE:
Best Local Similarity
Matches 74; Conserv
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ORGANISM: Human
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US-09-799-799-3
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963 GCGAGCGCATAAATTCTGATTCCTGCCTGCCGGACAATTTATCTTTGGGGAGGCGG 1022
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APPLICANT: Lilie, James
APPLICANT: Wangy Youzhen
APPLICANT: Wangy Youzhen
APPLICANT: Wangy Youzhen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: THERAPY OF BREAST CANCER
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT FILING DATE: 2002-07-18
PRIOR PLLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                  / Match 3.3%; Score 37; DB 18; Length 421; Local Similarity 53.9%; Pred. No. 0.44; Pred. 76; Conservative 0; Mismatches 65; Indels
; OTHER INFORMATION: Clone ID: PAT_MRT3847_100348C.1
US-10-424-599-385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12351, Application US/10198846, Publication No. US20030099974A1, GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 719, Application US/10481032A

Publication No. US20050177901A1

GENERAL INFORMATION:

APPLICANT: Zhu, Tong

APPLICANT: Cheng, Wengiong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          987 GCCTGCCTGCCGGACAATTTA 1007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             218 TGCCCCCGGTTAAACAACATA 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | FEATURE: | NAME/KEY: misc_feature | LOCATION: 1, 2, 3, 4 | CTHER INFORMATION: n = A,T,C or G US-10-198-846-12351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 57.5
Matches 65; Conservative
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ORGANISM: Homo sapiens
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US-10-425-115-76475
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   APPLICANT: Briggs, seeven.
APPLICANT: Cooper, Bret
APPLICANT: Cooper, Bret
APPLICANT: Cooper, Stephen A.
APPLICANT: Goff, Stephen A.
APPLICANT: Moughamer, Todd
APPLICANT: Ratagiri, Funiaki
APPLICANT: Katagiri, Funiaki
APPLICANT: Kreps, Joel
APPLICANT: Ricke, Darrell
TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
FILE REFERENCE: 6014805PCT
CURRENT APPLICATION NUMBER: US 60/300,112
FRIOR PLILNG DATE: 2003-12-16
FRIOR APPLICATION NUMBER: US 60/325,277
FRIOR PLILNG DATE: 2001-06-22
FRIOR PLILNG DATE: 2001-12-20
FRIOR APPLICATION NUMBER: US 60/342,327
FRIOR APPLICATION NUMBER: US 60/342,327
FRIOR PLILNG DATE: 2001-06-22
FRIOR APPLICATION NUMBER: PCT/IB02/02450
FRIOR PLING DATE: 2001-12-20
FRIOR PLING DATE: 2001-12-20
FRIOR APPLICATION NUMBER: PCT/IB02/02450
FRIOR APPLICATION NUMBER: PCT/IB02/02450
FRIOR APPLICATION NUMBER: DCT/IB02/02450
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APPLICANT: JIANG, NING
APPLICANT: JIANG, NING
APPLICANT: JANG, XIAOYU
APPLICANT: EDDY, SEAN R.
TITLE OF INVENTION: TRANSPOSABLE ELEMENTS IN RICE AND METHODS OF USE
FILE REFERENCE: 18465-0018
CURRENT APPLICATION NUMBER: US/10/346,198
CURRENT FILING DATE: 2003-01-16
PRIOR PELING DATE: 2003-01-16
PRIOR FILING DATE: 2002-05-01
NUMBER OF SEQ ID NOS: 149
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      344 CCGTTTAGAGCAAGTATAATAAGTCCTAGTCAGCTGGCTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              404 AATCCTTAAACTGGAGGAGAAAGAAAGTAGGAG 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52 charc-reactropagoacacacacaaaaacaa 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.3%; Score 36.2; DE 68.8%; Pred. No. 1.9; iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 22, Application US/10346198; Publication No. US20040043485A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 59.0
Matches 62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
Briggs, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-346-198-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Oryza sativa
US-10-481-032A-719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 64; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-346-198-22/c
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GENERAL INFORMATION:
| Publication No. US20040234960A1
| CENERAL INFORMATION:
| Publication No. US20040234960A1
| GENERAL INFORMATION:
| APPLICANT: Alexander Olek
| APPLICANT: Christian Piepenbrock
| APPLICANT: Kurt Berlin
| TITLE OF INVENTION: Method for determining the degree of methylation of defined
| TITLE OF INVENTION: Method for determining the sequence context of 5'-CpG-
| TITLE OF INVENTION: We not sequence context of 5'-CpG-
| TITLE OF INVENTION: UNMBER: US/10/363,345A
| CURRENT APPLICATION NUMBER: US/10/363,345A
| CURRENT PILING DATE: 2003-03-03
| SEQ ID NO: 40712
| SEQ ID NO: 8601
                                                                                                                                                              Sequence 76475, Application US/10425115
5 Sequence 76475, Application US/10425115
7 ENDILCALION NO. US20040214272A1
7 ENDILCALT: La Rosa, Thomas J.
7 APPLICANT: La Rosa, Thomas J.
7 APPLICANT: Zhou, Yihua
7 APPLICANT: Zhou, Yihua
7 APPLICANT: Cao, Yonghua
7 TITLE OF INVENTION: Plants
7 TITLE OF INVENTION: Plants
7 TITLE OF INVENTION: US/10/425,115
7 CURRENT APPLICATION NUMBER: US/10/425,115
7 CURRENT FILING DATE: 2003-04-28
7 UNDER OF SEQ ID NOS: 369326
7 EBNGTH: 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 GATTCTGATCGTACCGCCGGTGGACTACCGCTTGAGTTGGCAGAGACTTGACAGTGG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTHER INFORMATION: Chemically treated genomic DNA (Homo sapiens); OTHER INFORMATION: CpG-island No: 18601
US-10-363-345A-18601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 35; DB 20; Length 704;
Pred. No. 2.7;
0; Mismatches 50; Indels
                           5855 GAAAGGAAAGAGAAAAGCGGGCGCATGTTTAATCGACAGC 5811
426 GAAAGTAGGAGTGAGAAGGGCGTCGGCGTTCGTCAATCGCTAGC 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 35.2; DB 20;
Pred. No. 1.5;
0; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Zea mays
FEATURE:
COTHER INFORMATION: Clone ID: MRT4577_169773C.1
US-10-425-115-76475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1040 AGCCCACAAGGCAACA 1055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 CTCCAACAAGGCAACA 137
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Best Local Similarity 56.5%;
Matches 65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 3.2%;
Best Local Similarity 53.7%;
Matches 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-363-345A-18601/c
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Search completed: August 30, 2005, 16:45:49 Job time : 861 secs



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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model Run on:

August 30, 2005, 12:51:04; Search time 4252 Seconds (without alignments) 9945.767 Million cell updates/sec

US-09-979-549-2 1111 Title: Perfect score:

1 gaagtcagaaggccgttcag......ccgagaagagagagagagag 1111 Sequence:

34239544 segs, 19032134700 residues IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

seq length: 0 seq length: 200000000 Minimum DB E Maximum DB E

Total number of hits satisfying chosen parameters:

Searched:

68479088

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 sv

summaries

EST:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	CK213031 FGAS02493	CD867573 AZO2.106K	CD867174 AZO2.105J	CAS93541 wpalc.pk0	CD938039 OV.108O07	CD865240 AZO2.073I	CA712930 wdk3c.pk0	œ	CK211149 FGAS02298	CK158306 FGAS03954	CK158740 FGAS04003	BQ805515 WHE3567 H	CK158414 FGAS03966	CD887850 G118.106G	CD874126 AZO3.101H	CD930486 GR45.111H	CA597581 wpa1c.pk0	CA598930 wyrlc.pk0		CA717478 wdk4c.pk0	CD922551 G750.103K	CF132917 WHE4351 G	CD894217 G118.125L	CA701748.wkm2c.pk0
	ΩI	CK213031	CD867573	CD867174	CA593541	CD938039	CD865240	CA712930	CK159678	CK211149	CK158306	CK158740	BQ805515	CK158414	CD887850	CD874126	CD930486	CAS97581	CA598930	CD884411	CA717478	CD922551	CF132917	CD894217	CA701748
	DB	7	9	ø	ø	9	ø	9	7	7	7	7	Ŋ	7	9	9	9	9	9	9	9	9	7	9	9
	Query Match Length DB	1061	509	570	594	631	624	430	875	1141	839	889	628	867	591	644	630	614	552	643	567	490	642	712	556
۰ (Query	3.6	8.9	8.9	8.3	8.3	8.1	7.9	7.2	7.1	7.0	6.9	6.5	6.4	6.3	6.2	6.1	9.0	0.9	5.9	5.9	5.8	5.8	5.8	5.7
	Score	105.6	66	66	92	92	90	88	79.8	79	78.2	77.2	72.4	70.6	9.69	9.89	67.6	67.2	66.2	99	65.2	64.6	64.6	64.4	63
	No.	7	7	М	4	S	y	7	6 0	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24
	Result No.	υ							υ	υ	υ	υ		υ											

CD904051 G356.112E	BE419251 WWR021.H3	BJ257084 BJ257084	BJ221033 BJ221033	AL821755 AL821755	BE419352 WWS01.A5R	BJ253061 BJ253061	CL901946 CSHC1321	BE406240 WHE0409 D	BJ239800 BJ239800	BJ233935 BJ233935	CA098733 SCRLCL603	BJ273554 BJ273554	BU101004 WHE3360 F	BJ320546 BJ320546	CK158744 FGAS04003	CA497278 WHE3225 C	CL752059 OR BBa011	BJ296612 BJ296612	BJ290275 BJ290275	BJ262654 BJ262654
CD904051	BE419251	BJ257084	BJ221033	AL821755	BE419352	BJ253061	CL901946	BE406240	BJ239800	BJ233935	CA098733	BJ273554	BU101004	BJ320546	CK158744	CA497278	CL752059	BJ296612	BJ290275	BJ262654
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63	62	62	62	61.2	61	9	59.2	58.8	58	28	58	57.8	57.8	57.8	57.4	56.4	55.6		55	24
25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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ALIGNMENTS

RESULT 1

	CK213031 1061 bp mRNA linear BST 09-DEC-2003	reasuzasso iricicum descivum reas: miniary o car caib i iillicum destivum cDNA, mRNA sequence.	CK213031	CK213031.1 GI:39619135	EST.	Triticum aestivum (bread wheat)	Triticum aestivum	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;	Pooideae; Triticeae; Triticum.	1 (bases 1 to 1061)	Allard, F., Crosby, W.L., Danyluk, J., Eudes, F., Frick, M., Gaudet, D.,	Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A.,	Links, M.G., McCarthy, E.L., Monroy, A., Muzak, I., Nilson, D.,	Penniket, C., Roach, J.L. and Sarhan, F.	Functional Genomics of Abiotic Stress In Wheat and Canola Crops	Unpublished (2003)	Contact: Wm L Crosby	Bioinformatics	University of Saskatchewan, Department of Computer Science	1C101 Engineering Building, 57 Campus Drive, Saskatoon,	Saskatchewan, S7N 5A9, Canada	Tel: 306 966 1769	Fax: 306 966 2033	Email: fgas ests@cs.usask.ca	This sequence is the direct result of the Base calling software	Phred (default parameters). It is the raw base calls. To aid in the	(default parameters) has been run on this sequence. Lucy identified	Plate: L6B007 row: O column: 02.	Location/Qualifiers	1. 1061
CK213031/c	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM				REFERENCE	AUTHORS				TITLE	JOURNAL	COMMENT												FEATURES	source

/mol Lyppanian 1112 cm. 1251.2 cm. 1251.2 cm. 1251.2 cm. 1252.2 cm 'organism="Triticum aestivum"

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99; Conservative
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AZO2.106K05F001108 AZO2 Triticum aestivum cDNA clone AZO2106K05,
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooldeae; Triticeae; Triticum.
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Contact: Genoplante
Genoplante
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9.5%; Score 105.6; DB 7; Length 1061;
Best Local Similarity 96.4%; Pred. No. 3.7e-20;
Matches 108; Conservative 0; Mismatches 4; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
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/cultivar="recital"
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Triticum aestivum
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/tissue_type="root"
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CD867573
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KEYWORDS
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Length 509;

DB 6; 3e-18;

8.9%; Score 99; 100.0%; Pred. No.

Query Match Best Local Similarity

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594 bp mRNA linear EST 21-NOV-2002 wpalc.pk002.p19 wpalc Triticum aestivum cDNA clone wpalc.pk002.p19 5′ end, mRNA sequence.
CA593541
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                                   1013 GGGGAGGCGGGGATTGGAGACAGAGCCCACAAGGCAACAACAAGTGCGCGTGAGA 1072
                                                                                                                                                                                                                                                         CD867174 STO bp mRNA linear EST 11-JUL-2003
AZO2.105J01F001124 AZO2 Triticum aestivum CDNA clone AZO2105J01,
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Triticum aestivum
Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooldeae; Triticeae; Triticum.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
(bases 1 to 570)
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Contact: Genoplante
Genoplante
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8.9%; Score 99; DB 6; Length 570;
Best Local Similarity 100.0%; Pred. No. 3.1e-18;
Matches 99; Conservative 0; Mismatches 0; Indels
0; Indels
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                                                                                                                       1073 AATCAACAAGCGGTGCTTGCCGAGAAGAGAGAGAGAG 1111
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    0; Mismatches
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/clone="AZO2105J01"
/tissue type="roct"
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Triticum aestivum
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CD867174.1 GI:32550990
                                                                                                                                                                                                                                                                                                           mRNA sequence.
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wdk3c.pk008.e19 wdk3c Triticum aestivum cDNA clone wdk3c.pk008.e19 5' end, mRNA sequence. CA712930 CA712930.1 GI:25434723 EST.
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AZO2.073123F000912 AZO2 Triticum aestivum CDNA clone AZO2073123,
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
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Unpublished (2003)
Contact: Genoplante
Genoplante
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Location/Qualifiers
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                                                         Query Match 8.3%; Score 92; DB 6; Length 631; Best Local Similarity 100.0%; Pred. No. 4.3e-16; Matches 92; Conservative 0; Mismatches 0; Indels
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
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Genoplante.
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CD865240
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KEYWORDS
SOURCE
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Pooideae, Triticeae, Triticum.
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XhoI; Wheat (Triticum aestivum) pre-meiotic anthers JIC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
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Unpublished (2003)
  1 (bases 1 to 594)
Tingey,S.V., Moore,G., Griffiths,S., Powell,W., Wolters,P.,
Dolan,M., Hainey,C., Miao,G., Caraher,N. and Hanafey,M.K.
DuPont Wheat cDNA Sequence in collaboration with the John Innes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CD938039 631 bp mRNA linear EST 15-JUL-;
OV.108007F010206 OV Triticum aestivum cDNA clone OV108007, mRNA
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                                                                               Center 1
Uppublished (2002)
Uppublished (2002)
Contact: Scott V. Tingey
Corp Genetics
E. I DuPont de Nemours and Company
I Innovation May, P.O. Box 6104, Newark, DE 19714-6104, USA
Tel: 302-631-2607
Fax: 302-631-2607
Email: Scott.V.Tingey@USA.dupont.com
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100.0%; Pred. No. 4.2e-16;
tive 0; Mismatches 0; Indels
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Triticum aestivum
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Contact: Wm L Crosby
Bioinformatics
Unpublished (2003)
Contact: Wm L Crosby
Bioinformatics
University of Saskatchewan, Department of Computer Science
University of Saskatchewan, 570 Sappus Drive, Saskatoon,
Saskatchewan, S7N SA9, Canada
Tel: 306 966 1769
Fax: 306 966 2033
Email: fgas ests@cs.usask.ca
This sequence is the direct result of the Base calling software
Phred (default parameters). It is the raw base calls. To aid in the identification of the high quality insert the software Lucy (default parameters) has been run on this sequence. Lucy identified the reference in the result of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence is the direct result of the Base calling software phred (default parameters). It is the raw base calls. To aid in the identification of the high quality insert the software Lucy (default parameters) has been run on this sequence. Lucy identified the region [123,778].

Plate: Talt540 row: B column: 16.
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Matches 84; Conservative 0; Mismatches 8;
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aestivum cDNA, mRNA sequence.
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/note="Vector: pBluescript SK+; Site_1: EcoRI; Site_2:
XhoI; Wheat (Triticum aestivum L.) developing kernel, 14
days after anthesis."
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E. I. DuPont de Nemours and Company
Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
Tel: 302-631-2607
Fax: 302-631-2607
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/mol_type="mRNA"
/db_xref="taxon:4565"
/clone="wdk3c.pk008.e19"
/tissue_type="kernel"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: Scott.V.Tingey@USA.dupont.com
Seq primer: M13.
Location/Qualifiers
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Triticum aestivum
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/Glone lib="Triticum aestivum FGAS: Library 6 CAP GATE 1"
/Glone lib="Triticum aestivum FGAS: Library 6 CAP GATE 1"
/Glone lib="Triticum aestivum FGAS: Library 6 CAP GATE 1"
/Soth and leaf (50%) tissues from wheat cultivar Norstear after short exposure times to low temperature in the light and in the dark. 12 mRNA populations were combined before constructing the library. The first 6 populations: After 7 days of growth at 20Cs from wheat cultivar Norstear after short exposure times to low temperature in the light and in the dark. 12 mRNA populations were combined before constructing the library. The first 6 populations: After 7 days of growth at 20, wheat plants were transferred to 4C in the light. 1cm crown sections and green leaf tissu were separately harvested after 1, 3, and 6 hours of low temperature exposure. The last 6 populations: After 7 days of growth at 20C, wheat plants were transferred to 4C in the dark. 1cm crown sections and green leaf tissu were separately harvested after 1, 3, and 6 hours of low temperature exposure. First strand synthesis in this library was done in the presence of methylated ACTP thereby protecting from internal cleavage with NotI. In addition, this library used a primer for second strand synthesis that annealed to an artificial sequence (RNA) allow and an entable of the presence of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oligo) added before first strand synthesis. Therefore when
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1 (bases 1 to 839)
Allard,F., Crosby,W.L., Danyluk,J., Eudes,F., Frick,M., Gaudet,D., Genswein,B., Graf,R., Gulick,P., Hyroan,L.D., Laroche,A., Links,M.G., McCarthy,L., Monroy,A., Muzak,I., Nilson,D., Punctional Genomics of Abiotic Stress In Wheat and Canola Crops Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequences from EST generated from this library will be masked for vector and adaptor sequences, an additional masking step will have to be included to mask this RNA oligo that is common to all clones (sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CK158306
FGASO39543 Triticum aestivum FGAS: TaLt5 Triticum aestivum cDNA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 7.1%; Score 79; DB 7; Length 1141; Best Local Similarity 91.4%; Pred. No. 4.4e-12; Matches 96; Conservative 0; Mismatches 5; Indels
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Triticum aestivum
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CK158306.1 GI:38983324
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/organism="Triticum aestivum"
/mol_type="mRNA"
/mol_type="mRNA"
/mol_type="mRNA"
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/note="Organ: Crown; Vector: pGEM-T; SSH (suppression subtractive hybridization) cDNA library from genotype pl178383 cold hardened at 2 C for 21 days and 49 days (equal amount of cDNA pooled together before subtraction, tester) and subtracted against genotype Norstar cold hardened at 2 C for 1 day (24 H) (driver). Modified Smart cDNA (Clontech) priming and non-directional cloning"
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University of Saskatchewan, Department of Computer Science
1C101 Engineering Building, 57 Campus Drive, Saskatoon,
Saskatchewan, S7N 5A9, Canada
Tel: 306 966 1769
Fax: 306 966 2033
Email: fgas estages.usask.ca
This sequence is the direct result of the Base calling software
Phred (default parameters). It is the raw base calls. To aid in the
identification of the high quality insert the software Lucy
(default parameters) has been run on this sequence. Lucy identified
the region [125,709].
This sequence is the direct result of the Base calling software Phred (default parameters). It is the raw base calls. To aid in the identification of the high quality insert the software Lucy (default parameters) has been run on this sequence. Lucy identified the region [127, 643].

Plate: Talt534 row: A column: 15.

Location/Qualifiers
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FGAS040031 Triticum aestivum FGAS: Talt5 Triticum aestivum CDNA,
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(Dases 1 to 889)
Allard, F., Crosby, W.L., Danyluk, J., Eudes, F., Frick, M., Gaudet, D., Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A., Links, M.G., McCarthy, E.L., Monroy, A., Muzak, I., Nilson, D., Penniket, C., Roach, J.L. and Sarhan, F.
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CK158740.1 GI:38984191
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Contact: Wm L Crosby
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Best Local Similarity
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ORIGIN

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/mo.Lype="mix.nx."
/cultivar="Wheat line PI 178383"
/db xref="taxon:4565"
/lab host="halfs alpha"
/clone_lib="Triticum astivum FGAS: Talt5"
/note="Organ: Crown: Vector: pGEM-T; SSH (suppression subtractive hybridization) cDNA library from genotype PI178383 cold hardened at 2 C for 21 days and 49 days (equal amount of CDNA pooled together before subtraction, tester) and subtracted against genotype Norstar cold hardened at 2 C for 1 day (24 H) (driver). Modified Smart cDNA (Clontech) priming and non-directional cloning"
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US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center 800 Buchanan Street, Albany, CA 94710, USA
Pax: 5105595773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BQ805515 628 bp mRNA linear BST 31-JUL-2002 WHE3567_H02_003ZS Wheat developing grains cDNA library Triticum assetivum cDNA clone WHE3567_H02_003, mRNA sequence.
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/dev stage="3-44 days post anthesis seed"
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/clone_lib="Wheat developing grains cDNA library"
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EcoRI; Plants were grown under six following different
envizonmental regimes in greenhouse, Envizonment 1)
24oC/17oC day/night, well-watered, with post-anthesis
fertilizer, Environment 2) 24oC/17oC day/night,
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/organism="Triticum aestivum"
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Triticum aestivum
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/cultivar="Butte 86"
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type="mRNA"
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BQ805515.1 GI:22029724
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BQ805515
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well-watered, without post-anthesis fertilizer,
Environment 3) 370C/170C day/night, well-watered, with
post-anthesis fertilizer, Environment 4) 370C/170C
day/night, well-watered, without post-anthesis fertilizer,
Environment 5) 370C/170C day/night plus drought, with
post-anthesis fertilizer. Environment 6) 370C/170C
day/night plus drought, without post-anthesis fertilizer,
day/night liquid nitrogen, Environment at 3, 5, 7,
8, 10, 12, 16, 20, 24, 28, 32, 36, 40, 44 DPA Environment
2 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 32, 34 DPA Environment 5 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA and total RNA was prepared by
S. Altenbach and K. Cronin at USDA-ARS, Albany, CA. A
clones were in vivo excised to give pBluescript SK(-)
phagemids in the TO Close lab (Chin, Close, Fenton) at
the University of California, was propered of the phase of the control of the University of California, was neaded.
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University of Saskatchewan, Department of Computer Science
Uci01 Engineering Building, 57 Campus Drive, Saskatcon,
Saskatchewan, S77 SA9, Canada
Tel: 306 966 1769
Fax: 306 966 2033
Email: fgas ests@cs.usask.ca
This sequence is the direct result of the Base calling software
Phred (default parameters). It is the raw base calls. To aid in the
identification of the high quality insert the software Lucy
(default parameters) has been run on this sequence. Lucy identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST 05-DEC-2003
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1 (Dases 1 to 867)
Allard,F., Crosby,W.L., Danyluk,J., Eudes,F., Frick,M., Gaudet,D., Genswain,B., Gaff,R., Gulick,P., Hrycan,L.D., Laroche,A., Eninks,M.G., McCarthy,E.L., Monroy,A., Muzak,I., Nilson,D., Penniket,C., Roach,J.L. and Sarhan,F.

Punctional Genomics of Abiotic Stress In Wheat and Canola Crops Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    preparations and DNA sequencing were performed in the OD Anderson lab (others)."
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TaLt5 Triticum aestivum cDNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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98.6%; Pred. No. 3.7e-10;
iive 0; Mismatches 1;
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Plate: TaLt534 row: I column: 10.
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FGAS039669 Triticum aestivum FGAS:
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Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA sequence.
CK158414
CK158414.1 GI:38983539
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Best Local Similarity 98...
Loca 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 AGAGAGAGAGAG 74
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KEYWORDS
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Location/Qualifiers

FEATURES

us-09-979-549-2.rst

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Search completed: August 30, 2005, 16:27:31 Job time : 4256 secs
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Matches 85; Conserv
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AUTHORS
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                                                                                          RESULT 15
CD874126
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SOURCE
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           // mol_type="mRNA"
// ultivar="Wheat line PI 178383"
// db Aref="Laxon:4565"
// db Aref="Croun; Vector: pGBM-T; SSH (suppression subtractive hybridization) cDNA library from genotype PI178383 cold hardened at 2 C for 21 days and 49 days (equal amount of cDNA pooled together before subtraction, tester) and subtracted against genotype Norstar cold hardened at 2 C for 1 day (24 H) (driver). Modified Smart cDNA (Clontech) priming and non-directional cloning"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       591 bp mRNA linear EST 14-JUL-2003 G118106G24F010606 G118 Triticum aestivum cDNA clone G118106G24, CD887850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1018 GGCGGGCCGGGATTGGAGACAGAGCCCACAAGGCAACAACAAGTGCGCGTGAGAAATCA 1077
                                                                                                                                                                                                                                                                                                                                                                                              778
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Poideae, Triticeae, Triticum.
1 (bases 1 to 591)
Genoplante.
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Location/Qualifiers
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pollination)"
/clone_lib="G118"
                                                                                                                                                                                                                                                                            Score 70.6; DB 7; Length 867;
Pred. No. 1.4e-09;
0; Mismatches 9; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
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Pred. No. 2.6e-09;
0; Mismatches 4;
organism="Triticum aestivum"
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                                                                                                                                                                                                                                                                                                                                                                                                                                   1087 GCTTGCCGAGAGAGAGAGAGAGAGAG 1111
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/clone="G118106G24"
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/cultivar="recital"
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Best Local Similarity 89.4%;
Matches 76; Conservative (
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ilarity 91.5%;
Conservative
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CD887850
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CD874126 644 bp mRNA linear EST 11-JUL-2003
AZO3.101H05F010928 AZO3 Triticum aestivum cDNA clone AZO3101H05,
mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
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rel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genonics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
Location/Qualifiers
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Unpublished (2003)
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1078 ACAAGCGGTGCTTGCCGAGAAGAGAGAGAGAGAG 1111
                                                    69 -- AAGCGGTGCTTGCCGAGAGAGAGAGAGAG 100
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/mol type="mRNA"
/cultivar="recital"
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Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:4565"
/clone="AZO3101H05"
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/clone_lib="AZO3"
                                                                                                                                                                                                                                                                                         CD874126.1 GI:32557942
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Genoplante
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